

OM protein - protein search, using sw model

Run on: June 24, 2004, 15:54:37 ; Search time 43.05 Seconds
 (without alignments)
 4069.212 Million cell updates/sec

Title: US-10-054-680-4
 Perfect score: 3228
 Sequence: 1 MAWLRLQPLTSAFLHFGGLVT.....ADYGRRGGQEDSRDGKASIG 620

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3228	100.0	620	5	ABB81914	Abb81914 Human ion
2	3093	95.8	595	6	ABR40134	Abr40134 Human 690
3	3093	95.8	921	5	ABP74104	Abp74104 Human TRI
4	3093	95.8	921	5	ABB83246	Abb83246 Human tra
5	3093	95.8	921	5	ABB81913	Abb81913 Human ion
6	3093	95.8	921	5	ABB81915	Abb81915 Human ion
7	3093	95.8	922	5	ABB81916	Abb81916 Human ion
8	3093	95.8	922	5	ABB81917	Abb81917 Human ion
9	3093	95.8	925	6	ABU12042	Abu12042 Human NOV

10	3093	95.8	927	5	AAM47745	Aam47745	Human nat
11	3093	95.8	928	6	ABU12041	Abu12041	Human NOV
12	3016	93.4	927	5	ABB83247	Abb83247	Human tra
13	2940	91.1	895	6	ABU12043	Abu12043	Human NOV
14	2147.5	66.5	970	5	AAE18291	Aae18291	Bovine NC
15	2143.5	66.4	609	4	AAM13701	Aam13701	Peptide #
16	2143.5	66.4	609	4	ABB32633	Abb32633	Peptide #
17	2143.5	66.4	609	4	AAM26102	Aam26102	Peptide #
18	2143.5	66.4	609	4	ABB18131	Abb18131	Protein #
19	2143.5	66.4	609	4	AAM53461	Aam53461	Human bra
20	2143.5	66.4	609	4	ABG47486	Abg47486	Human liv
21	2143.5	66.4	609	5	ABG35474	Abg35474	Human pep
22	1961	60.7	921	7	AAO27170	Aao27170	Human 465
23	1961	60.7	952	3	AAB41497	Aab41497	Human ORF
24	1339.5	41.5	950	4	ABB61721	Abb61721	Drosophil
25	362.5	11.2	539	3	AAY58044	Aay58044	Arabidops
26	203.5	6.3	106	6	ABR40136	Abr40136	69039 pro
27	203.5	6.3	618	4	AAM78712	Aam78712	Human pro
28	203.5	6.3	661	5	ABB84485	Abb84485	Human NCK
29	203.5	6.3	661	6	AAO29752	Aao29752	Human 577
30	203.5	6.3	661	7	ADE54756	Ade54756	Human Pro
31	202	6.3	6304	6	ABU09236	Abu09236	Human neu
32	201.5	6.2	670	7	ADE54754	Ade54754	Rat Prote
33	197	6.1	546	4	ABB12262	Abb12262	Human ver
34	186.5	5.8	644	7	ADE31661	Ade31661	Human 692
35	184	5.7	2092	6	ABU09234	Abu09234	Rat neuro
36	180.5	5.6	603	5	AAE22088	Aae22088	Human nov
37	172.5	5.3	630	5	ABP69673	Abp69673	Human pol
38	171.5	5.3	2071	4	AAE10949	Aae10949	Mouse mas
39	171.5	5.3	2780	4	AAE10924	Aae10924	Mouse mon
40	162.5	5.0	856	4	ABB60425	Abb60425	Drosophil
41	161	5.0	759	5	ABG61545	Abg61545	Human tra
42	161	5.0	2701	5	ABP74125	Abp74125	Human TRI
43	161	5.0	2753	6	ADA05806	Ada05806	Human NOV
44	161	5.0	2753	6	ADA05800	Ada05800	Human NOV
45	161	5.0	3838	6	ADA05802	Ada05802	Human NOV

ALIGNMENTS

RESULT 1

ABB81914

ID ABB81914 standard; protein; 620 AA.

XX

AC ABB81914;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #2.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral.

XX

OS Homo sapiens.

XX

PN WO200259316-A2.

XX
 PD 01-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001817.
 XX
 PR 23-JAN-2001; 2001US-0263384P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Friddle CJ, Hilbun E;
 XX
 DR WPI; 2002-599791/64.
 DR N-PSDB; ABQ78862.
 XX
 PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.
 XX
 PS Claim 4; Page 40-41; 42pp; English.
 XX
 CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence represents a NHIEP of the invention
 XX
 SQ Sequence 620 AA;

Query Match 100.0%; Score 3228; DB 5; Length 620;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRKKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRKKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN	300

Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQDLVEMANYYALSHQQKSRIFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQDLVEMANYYALSHQQKSRIFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVCDRQE	600
Db	541	VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVCDRQE	600
Qy	601	ADYGRRGGQEDSRDGKASIG	620
Db	601	ADYGRRGGQEDSRDGKASIG	620

RESULT 2

ABR40134

ID ABR40134 standard; protein; 595 AA.
 XX
 AC ABR40134;
 XX
 DT 04-JUL-2003 (first entry)
 XX
 DE Human 69039 protein.
 XX
 KW Human; 69039; neuroprotective; gene therapy; haematopoietic disorder;
 KW Na⁺/Ca²⁺ exchanger; ion transporter; neural tissue;
 KW neurological disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO2003029410-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 27-SEP-2002; 2002WO-US030817.
 XX
 PR 28-SEP-2001; 2001US-0325737P.
 XX
 PA (MILL-) MILLENIUM PHARM INC.
 XX
 PI Carroll JM;
 XX
 DR WPI; 2003-381617/36.
 DR N-PSDB; ACC00414.
 XX
 PT Identifying a nucleic acid molecule associated with a disorder for

PT preparing a composition for treating hematopoietic or neurological
PT disorder by detecting the presence of a nucleic acid molecule in the
PT sample that is amplified.

XX

PS Example 1; Page 110; 133pp; English.

XX

CC The present sequence is the protein sequence for human 69039, a novel
CC Na⁺/Ca²⁺ exchanger family member (ion transporter). 69039 was shown to be
CC expressed in human haematopoietic cells, e.g. CD34-expressing progenitor
CC cells as well as in neural tissues, e.g. brain cortex and hypothalamus.
CC 69039 may therefore be used for preparing a composition for treating
CC haematopoietic or neurological disorder

XX

SQ Sequence 595 AA;

Query Match 95.8%; Score 3093; DB 6; Length 595;
Best Local Similarity 100.0%; Pred. No. 5.5e-308;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRITSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDET	595

RESULT 3

ABP74104

ID ABP74104 standard; protein; 921 AA.
 XX
 AC ABP74104;
 XX
 DT 30-JAN-2003 (first entry)
 XX
 DE Human TRICH SEQ ID NO 9.
 XX
 KW Human; TRICH; transporter and ion channel; transport disorder;
 KW cystic fibrosis; diabetes mellitus; Parkinson's disease; cancer;
 KW neurological disorder; Alzheimer's disease; Huntington's disease;
 KW immunological disorder; AIDS; asthma; cell proliferative disorder;
 KW transgenic; gene therapy; neuroprotective; antidiabetic; cytostatic;
 KW antiparkinsonian; hypotensive; nootropic; antianaemic; anticonvulsant;
 KW cerebroprotective; cardiast; anti-HIV; human immunodeficiency virus;
 KW antiasthmatic; antiatherosclerotic; antigout; antiarteriosclerotic;
 KW hepatotropic; antiinflammatory; virucide; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200246415-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 05-DEC-2001; 2001WO-US046963.
 XX
 PR 08-DEC-2000; 2000US-0254303P.
 PR 15-DEC-2000; 2000US-0256190P.
 PR 21-DEC-2000; 2000US-0257504P.
 PR 12-JAN-2001; 2001US-0261546P.
 PR 19-JAN-2001; 2001US-0262832P.
 PR 26-JAN-2001; 2001US-0264377P.
 PR 02-FEB-2001; 2001US-0266019P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Lee EA, Baughn MR, Yue H, Ding L, Raumann BE, Hafalia AJA;
 PI Khan FA, Nguyen DB, Elliott VS, Ramkumar J, Walia NK, Ison CH;
 PI Lu Y, Gandhi AR, Warren BA, Duggan BM, Tribouley CM, Burford N;
 PI Lu DAM, Lal PG, Yao MG, Xu Y, Bruns CM, Thangavelu K, Swarnakar A;
 PI Tang YT, Azimzai Y, Thornton M, Arvizu C, Policky JL;
 XX
 DR WPI; 2002-519667/55.
 DR N-PSDB; ABZ33735.
 XX
 PT Novel human transporter and ion channel polypeptide, useful in diagnosis,
 PT prevention or treatment of transport, neurological, muscle, immunological
 PT and cell proliferative disorders.
 XX
 PS Claim 64; SEQ ID NO 9; 146pp + Sequence Listing; English.
 XX
 CC The invention relates to human transporter and ion channel polypeptide

CC (TRICH) (I) selected from one of 32 polypeptide sequences (ABP74096-
 CC ABP74127), a naturally occurring polypeptide comprising a sequence having
 CC at least sequence 90 % identity to (I) or a biologically active or
 CC immunogenic fragment of (I). (I) is useful for screening a compound for
 CC effectiveness as an agonist or antagonist, for screening a compound that
 CC specifically binds (I) or modulates the activity of (I) and for preparing
 CC a polyclonal or monoclonal antibody by hybridoma technology.
 CC Polynucleotides (II, ABZ33727-ABZ33758) encoding (I) are useful for
 CC screening a compound altering gene expression. (I) and (II) are useful in
 CC a diagnostic tests for a condition or a disease associated with the
 CC expression of TRICH in a biological sample, especially disorders selected
 CC from a transport disorder such as cystic fibrosis, diabetes mellitus,
 CC Parkinson's disease, cardiac disorders, neurological disorders such as
 CC Alzheimer's disease, Huntington's disease, muscle disorders,
 CC immunological disorder such as AIDS, asthma and atherosclerosis, and cell
 CC proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis and
 CC cancer. (II) is useful for creating knock-in humanised animals or
 CC transgenic animals to model human diseases, in somatic or germline gene
 CC therapy, to generate a transcript image of a tissue or cell type, for
 CC detecting differences in the chromosomal location due to translocation,
 CC inversion among normal, carrier or affected individuals and for mapping
 CC genomic sequences. Note: The sequence data for this patent is not
 CC represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 921 AA;

Query Match 95.8%; Score 3093; DB 5; Length 921;
 Best Local Similarity 100.0%; Pred. No. 1.1e-307;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420

Db 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
 |||

Db 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 |||

Db 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
 |||

Db 541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

RESULT 4

ABB83246

ID ABB83246 standard; protein; 921 AA.

XX

AC ABB83246;

XX

DT 21-AUG-2002 (first entry)

XX

DE Human transporter protein.

XX

KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
 KW spleen; testis; leukocyte; foetal brain; chromosome 14.

XX

OS Homo sapiens.

XX

PN WO200233086-A2.

XX

PD 25-APR-2002.

XX

PF 17-OCT-2001; 2001WO-US032152.

XX

PR 17-OCT-2000; 2000US-0240836P.

PR 13-MAR-2001; 2001US-00804474.

XX

PA (PEKE) PE CORP NY.

XX

PI Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;

PI Beasley EM;

XX

DR WPI; 2002-479677/51.

DR N-PSDB; ABN83428, ABN83429.

XX

PT Human transporter peptide related to sodium/calcium exchanger subfamily
 PT for identifying modulators useful for treating a disease or condition
 PT mediated by human transporter protein.

XX

PS Claim 1; Fig 2; 200pp; English.

XX

CC The present sequence is a human transporter protein, which is related to
 CC the sodium/calcium exchanger subfamily. Experimental data indicates
 CC expression of the transporter gene in humans in brain, heart, kidney,
 CC lung, spleen, testis, leukocyte and foetal brain. The gene of the

CC transporter was mapped to chromosome 14 by ePCR
XX
SQ Sequence 921 AA;

Query Match 95.8%; Score 3093; DB 5; Length 921;
Best Local Similarity 100.0%; Pred. No. 1.1e-307;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAAFNMF 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAAFNMF 180

Qy    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360

Qy    361 MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy    541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET 595
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET 595
```

RESULT 5
ABB81913
ID ABB81913 standard; protein; 921 AA.
XX
AC ABB81913;
XX
DT 09-OCT-2002 (first entry)
XX

DE Human ion exchanger protein #1.
 XX
 KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral.
 XX
 OS Homo sapiens.
 XX
 PN WO200259316-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001817.
 XX
 PR 23-JAN-2001; 2001US-0263384P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Friddle CJ, Hilbun E;
 XX
 DR WPI; 2002-599791/64.
 DR N-PSDB; ABQ78861.
 XX
 PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.
 XX
 PS Claim 2; Page 37-39; 42pp; English.
 XX
 CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence represents a NHIEP of the invention
 XX
 SQ Sequence 921 AA;

Query Match 95.8%; Score 3093; DB 5; Length 921;
 Best Local Similarity 100.0%; Pred. No. 1.1e-307;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIDRVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIDRVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180

Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRIFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRIFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 6

ABB81915

ID ABB81915 standard; protein; 921 AA.

XX

AC ABB81915;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 Asp/Gly mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;

KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;

KW mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 630

FT /note= "Wild-type Asp substituted by Gly"

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Friddle CJ, Hilbun E;
XX
DR WPI; 2002-599791/64.
XX
PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.
XX
PS Disclosure; Page; 42pp; English.
XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 2 (ABB81913)
XX
SQ Sequence 921 AA;

Query Match 95.8%; Score 3093; DB 5; Length 921;
Best Local Similarity 100.0%; Pred. No. 1.1e-307;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRKHHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRKHHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420

Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 7

ABB81916

ID ABB81916 standard; protein; 922 AA.
 XX
 AC ABB81916;
 XX
 DT 09-OCT-2002 (first entry)
 XX
 DE Human ion exchanger protein #1 Ala mutant.
 XX
 KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 704. .705
 FT /note= "Wild-type Ala Ala substituted by Ala Ala Ala"
 XX
 PN WO200259316-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001817.
 XX
 PR 23-JAN-2001; 2001US-0263384P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Friddle CJ, Hilbun E;
 XX
 DR WPI; 2002-599791/64.
 XX
 PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.
 XX
 PS Disclosure; Page; 42pp; English.

XX
 CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence represents a mutant form of a NHIEP of the invention. Note: The
 CC present sequence is not shown in the specification but is derived from
 CC the human NHIEP sequence shown as SEQ ID 2 (ABB81913)
 XX
 SQ Sequence 922 AA;

Query Match 95.8%; Score 3093; DB 5; Length 922;
 Best Local Similarity 100.0%; Pred. No. 1.2e-307;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKRIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKRIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRITSGARGTVIVFPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 8

ABB81917

ID ABB81917 standard; protein; 922 AA.

XX

AC ABB81917;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 Asp/Gly+Ala mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
 KW mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 630

FT /note= "Wild-type Asp substituted by Gly"

FT Misc-difference 704. .705

FT /note= "Wild-type Ala Ala substituted by Ala Ala Ala"

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.

XX

PS Disclosure; Page; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence represents a mutant form of a NHIEP of the invention. Note: The
 CC present sequence is not shown in the specification but is derived from

CC the human NHIEP sequence shown as SEQ ID 2 (ABB81913)
XX
SQ Sequence 922 AA;

Query Match 95.8%; Score 3093; DB 5; Length 922;
Best Local Similarity 100.0%; Pred. No. 1.2e-307;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMF 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMF 180

Qy    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHHKRYRDKHKGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 FPVCVLLAWVADKRLLFYKYMHHKRYRDKHKGIIETEGDHPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRIFYRIQATR 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRIFYRIQATR 360

Qy    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDHF 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDHF 480

Qy    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy    541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
```

RESULT 9
ABU12042
ID ABU12042 standard; protein; 925 AA.
XX
AC ABU12042;
XX
DT 19-FEB-2003 (first entry)
XX

DE Human NOV1b CG56558-02 protein SEQ ID 4.
 XX
 KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200281625-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010366.
 XX
 PR 03-APR-2001; 2001US-0281086P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 06-APR-2001; 2001US-0282020P.
 PR 10-APR-2001; 2001US-0282930P.
 PR 12-APR-2001; 2001US-0283444P.
 PR 12-APR-2001; 2001US-0283512P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285381P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 25-APR-2001; 2001US-0286292P.
 PR 07-JUN-2001; 2001US-0296692P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 08-AUG-2001; 2001US-0311003P.
 PR 13-AUG-2001; 2001US-0311973P.
 PR 16-AUG-2001; 2001US-0312901P.
 PR 14-SEP-2001; 2001US-0322283P.
 PR 05-OCT-2001; 2001US-0327448P.
 PR 31-DEC-2001; 2001US-0345734P.
 PR 03-JAN-2002; 2002US-0345755P.
 PR 04-FEB-2002; 2002US-0354391P.
 PR 02-APR-2002; 2002US-00114153.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
 PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
 PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
 PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
 PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
 PI Mazur A;
 XX
 DR WPI; 2003-046862/04.
 DR N-PSDB; ABX56262.
 XX
 PT New isolated NOVX polypeptide useful for treating cardiomyopathy,

PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.

XX

PS Claim 1; Page 85; 425pp; English.

XX

CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments
CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306

XX

SQ Sequence 925 AA;

Query Match 95.8%; Score 3093; DB 6; Length 925;

Best Local Similarity 100.0%; Pred. No. 1.2e-307;

Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQQKSRAFYRIQATR	360

Qy 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
 |||
 Db 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
 |||
 Db 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy 481 FVRLSNVRIEEEQPEGMPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 |||
 Db 481 FVRLSNVRIEEEQPEGMPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
 |||
 Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

RESULT 10

AAM47745

ID AAM47745 standard; protein; 927 AA.

XX

AC AAM47745;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3.

XX

KW Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;
 KW cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;
 KW myocarditis; pulmonary hypertension; cardiotoxicity; cardiant; Vaccine;
 KW coronary heart disease; renal failure; ischaemic disorder;
 KW Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder.

XX

OS Homo sapiens.

XX

PN WO200183744-A2.

XX

PD 08-NOV-2001.

XX

PF 30-APR-2001; 2001WO-EP004886.

XX

PR 02-MAY-2000; 2000EP-00109080.

XX

PA (MERE) MERCK PATENT GMBH.

XX

PI Wilm C;

XX

DR WPI; 2002-041493/05.

DR

N-PSDB; ABA04756.

XX

PT New polypeptide, useful as vaccines for inducing immune response against
 PT diseases such as myocardial infarction, arrhythmia, ischemic disorders,
 PT renal disorders in mammal.

XX

PS Claim 1; Page 38-41; 41pp; English.

XX

CC The present sequence is the protein sequence for human Natrium(+)-Calcium

CC (2+) exchanger form 3 (HNCX3). The HNCX3 gene maps to human chromosome
CC 14. HNCX3 and its coding sequence are useful for treating acute and
CC chronic cardiac failure of different aetiologies, myocardial infarction,
CC cardiac hypertrophy, arrhythmia, myocarditis, pulmonary hypertension,
CC cardiotoxicity (e.g. induced by chemotherapy), coronary heart disease,
CC acute and chronic renal failure, ischaemic disorders of skeletal muscle
CC and ischaemic brain disorders of different aetiologies

XX

SQ Sequence 927 AA;

Query Match 95.8%; Score 3093; DB 5; Length 927;
Best Local Similarity 100.0%; Pred. No. 1.2e-307;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180

Qy    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR 360

Qy    361 MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy    541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
```

RESULT 11
ABU12041

ID ABU12041 standard; protein; 928 AA.
 XX
 AC ABU12041;
 XX
 DT 19-FEB-2003 (first entry)
 XX
 DE Human NOV1a CG56258-01 protein SEQ ID 2.
 XX
 KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200281625-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010366.
 XX
 PR 03-APR-2001; 2001US-0281086P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 06-APR-2001; 2001US-0282020P.
 PR 10-APR-2001; 2001US-0282930P.
 PR 12-APR-2001; 2001US-0283444P.
 PR 12-APR-2001; 2001US-0283512P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285381P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 25-APR-2001; 2001US-0286292P.
 PR 07-JUN-2001; 2001US-0296692P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 08-AUG-2001; 2001US-0311003P.
 PR 13-AUG-2001; 2001US-0311973P.
 PR 16-AUG-2001; 2001US-0312901P.
 PR 14-SEP-2001; 2001US-0322283P.
 PR 05-OCT-2001; 2001US-0327448P.
 PR 31-DEC-2001; 2001US-0345734P.
 PR 03-JAN-2002; 2002US-0345755P.
 PR 04-FEB-2002; 2002US-0354391P.
 PR 02-APR-2002; 2002US-00114153.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
 PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
 PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
 PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
 PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;

Db	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIE	TEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRR	MIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRR	MIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR		420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR		420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF		480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF		480
Qy	481	FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH		540
Db	481	FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH		540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV		595
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV		595

RESULT 12

ABB83247

ID ABB83247 standard; protein; 927 AA.

XX

AC ABB83247;

XX

DT 21-AUG-2002 (first entry)

XX

DE Human transporter protein-related protein, used in a homology alignment.

XX

KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;

KW spleen; testis; leukocyte; foetal brain; chromosome 14.

XX

OS Unidentified.

XX

PN WO200233086-A2.

XX

PD 25-APR-2002.

XX

PF 17-OCT-2001; 2001WO-US032152.

XX

PR 17-OCT-2000; 2000US-0240836P.

PR 13-MAR-2001; 2001US-00804474.

XX

PA (PEKE) PE CORP NY.

XX

PI Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;

PI Beasley EM;

XX

DR WPI; 2002-479677/51.

XX

PT Human transporter peptide related to sodium/calcium exchanger subfamily

PT for identifying modulators useful for treating a disease or condition

PT mediated by human transporter protein.

XX
 PS Disclosure; Fig 2; 200pp; English.
 XX
 CC The present invention relates to a human transporter protein, which is
 CC related to the sodium/calcium exchanger subfamily (ABB83246).
 CC Experimental data indicates expression of the transporter gene in humans
 CC in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal
 CC brain. The gene of the transporter was mapped to chromosome 14 by ePCR.
 CC The present protein was used in a sequence alignment with the transporter
 CC protein to illustrate the invention
 XX
 SQ Sequence 927 AA;

Query Match 93.4%; Score 3016; DB 5; Length 927;
 Best Local Similarity 97.1%; Pred. No. 9.5e-300;
 Matches 578; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

```

Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
      |||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGDLRDVPSAGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
      |||
Db     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
      |||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180

Qy    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF 240
      |||
Db    181 IIGICVYVIPDGETRRIKHLRVFFVTAAWSVFAYIWLYMILAVFSPGVVQWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
      |||
Db    241 FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIETEGEHPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRFYRIQATR 360
      |||
Db    301 LIPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRFYRIQATR 360

Qy    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      |||
Db    361 MMTGAGNILKKHAAEQAKKTASMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
      |||
Db    421 KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy    481 FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
      |||
Db    481 FVRLSNVRVEEQLEEGMTPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy    541 VSESIGVMEVKVLRITSGARGTVIVPFRFVEGTAKGGGEDFEDTYGELEFKNDETV 595
      |||
Db    541 VSESIGVMEVKVLRITSGARGTVIVPFRFVEGTAKGGGEDFEDTYGELEFKNDETV 595

```


RESULT 13

ABU12043

ID ABU12043 standard; protein; 895 AA.

XX

AC ABU12043;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human NOV1c 248057963 protein SEQ ID 6.

XX

KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;

KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;

KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;

KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;

KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;

KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;

KW metabolic syndrome X; wasting disease.

XX

OS Homo sapiens.

XX

PN WO200281625-A2.

XX

PD 17-OCT-2002.

XX

PF 03-APR-2002; 2002WO-US010366.

XX

PR 03-APR-2001; 2001US-0281086P.

PR 05-APR-2001; 2001US-0281906P.

PR 06-APR-2001; 2001US-0282020P.

PR 10-APR-2001; 2001US-0282930P.

PR 12-APR-2001; 2001US-0283444P.

PR 12-APR-2001; 2001US-0283512P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283710P.

PR 17-APR-2001; 2001US-0284234P.

PR 19-APR-2001; 2001US-0285325P.

PR 20-APR-2001; 2001US-0285381P.

PR 24-APR-2001; 2001US-0286068P.

PR 25-APR-2001; 2001US-0286292P.

PR 07-JUN-2001; 2001US-0296692P.

PR 26-JUN-2001; 2001US-0300883P.

PR 08-AUG-2001; 2001US-0311003P.

PR 13-AUG-2001; 2001US-0311973P.

PR 16-AUG-2001; 2001US-0312901P.

PR 14-SEP-2001; 2001US-0322283P.

PR 05-OCT-2001; 2001US-0327448P.

PR 31-DEC-2001; 2001US-0345734P.

PR 03-JAN-2002; 2002US-0345755P.

PR 04-FEB-2002; 2002US-0354391P.

PR 02-APR-2002; 2002US-00114153.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;

PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;

PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
 PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
 PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
 PI Mazur A;
 XX
 DR WPI; 2003-046862/04.
 DR N-PSDB; ABX56263.
 XX
 PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
 PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
 PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
 PT cancer.
 XX
 PS Claim 1; Page 86; 425pp; English.
 XX
 CC This invention describes novel polypeptides, termed NOVX which have
 CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
 CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
 CC cardiant and immunomodulatory activity. The polypeptide and any
 CC antibodies generated from it are useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease
 CC selected from a pathology associated with the NOVX polypeptide. Fragments
 CC and portions of the polynucleotides encoding NOVX polypeptides are useful
 CC to map the location of NOVX genes on a chromosome, to identify
 CC individuals from minute biological samples, as DNA markers for
 CC restriction fragment length polymorphism (RFLP), and are useful to
 CC prepare polymerase chain reaction primers. The products of the invention
 CC can be used in gene therapy and for treating cardiomyopathy, metabolic
 CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
 CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
 CC disease, immune disorders, haematopoietic disorders, and various
 CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
 CC syndrome X and wasting disorders associated with chronic diseases and
 CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments
 CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306
 XX
 SQ Sequence 895 AA;

Query Match 91.1%; Score 2940; DB 6; Length 895;
 Best Local Similarity 99.8%; Pred. No. 5.8e-292;
 Matches 565; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	30	AEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL	89
		:	
Db	2	SEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL	61
Qy	90	GVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEIL	149
Db	62	GVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEIL	121
Qy	150	LSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRRIKHLRVFFITA	209
Db	122	LSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRRIKHLRVFFITA	181
Qy	210	SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDK	269
Db	182	SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDK	241

Qy 270 HRGIIIEETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPE 329
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 242 HRGIIIEETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPE 301
 Qy 330 KDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD 389
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 302 KDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD 361
 Qy 390 EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDSKTMVVDYKTEDGSANAGADYEFT 449
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 362 EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDSKTMVVDYKTEDGSANAGADYEFT 421
 Qy 450 EGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP 509
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 422 EGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP 481
 Qy 510 RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTV 569
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 482 RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTV 541
 Qy 570 EGTAKGGGEDFEDTYGELEFKNDETV 595
 ||||||||||||||||||||
 Db 542 EGTAKGGGEDFEDTYGELEFKNDETV 567

RESULT 14

AAE18291

ID AAE18291 standard; protein; 970 AA.

XX

AC AAE18291;

XX

DT 07-MAY-2002 (first entry)

XX

DE Bovine NCX-1 protein.

XX

KW Bovine; recombinant protein; larvae expression system; membrane protein;
 KW transport protein; cardiac sodium-calcium exchange protein; Na-K ATPase;
 KW NCX1; cystic fibrosis transmembrane conductance regulator; CFTR; vaccine;
 KW channel forming protein; junctional protein; connexin 32.

XX

OS Bos taurus.

XX

PN WO200206464-A2.

XX

PD 24-JAN-2002.

XX

PF 09-JUL-2001; 2001WO-US021606.

XX

PR 13-JUL-2000; 2000US-0218125P.

XX

PA (UMOR) UNIV MISSOURI.

XX

PI Hale CC, Price EM;

XX

DR WPI; 2002-171806/22.

DR N-PSDB; AAD24450.

XX
PT Producing recombinant proteins e.g. membrane, transport and channel
PT forming proteins in larvae expression system, by infecting larvae with
PT vector having a sequence encoding recombinant fusion protein with
PT affinity tag.
XX
PS Example 1; Page 37-40; 40pp; English.
XX
CC The patent discloses methods of producing recombinant proteins in larvae
CC expression system, by infecting the larvae with vector having a sequence
CC encoding recombinant fusion protein with affinity tag. The methods are
CC useful for producing recombinant protein, preferably membrane proteins,
CC transport proteins such as NCX1 (cardiac sodium-calcium exchange protein)
CC or Na-K ATPase, channel forming proteins such as cystic fibrosis trans-
CC membrane conductance regulator (CFTR), junctional protein (conexin 32),
CC receptor, cytoskeletal and other membrane associated proteins. They are
CC also useful for producing prostate specific membrane antigens and sodium
CC phosphate co-transporters from kidney. The methods are also useful for
CC producing recombinant fusion proteins in large quantities that are both
CC highly homogenous and biologically active. The recombinant proteins
CC produced by the methods of the invention can be included as part of a
CC pharmaceutical, nutritional, drug or vaccine composition. The present
CC sequence is bovine NCX-1 protein
XX
SQ Sequence 970 AA;

Query Match 66.5%; Score 2147.5; DB 5; Length 970;
Best Local Similarity 69.4%; Pred. No. 1.8e-210;
Matches 422; Conservative 74; Mismatches 91; Indels 21; Gaps 8;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLF--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV	58
		: : : : : : :	
Db	1	MLQFSLSPTLSMGFHVIAVALLFSHVDHISAETEMEGEGNETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN	118
		: : : :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAAFNM	178
		: : : :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM	176
Qy	179	FIIIGICVYVIPDGETRKRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL	238
		: : : :	
Db	177	FIIIALCVYVVPDGETRKRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH	295
		: : : : : : :	
Db	237	FFFPICVVFVAVADRRLLFYKYVYKRYRAGKQGRGMIEHEGDRPSSKTEIEMDGKVNSH	296
Qy	296	---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ	348
		: : : : :	
Db	297	VDSFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355
Qy	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYYQC	407
		: : : : :	
Db	356	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTTEVAENDPVSKIFFEQGTYYQC	415

Qy 408 LENC GAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
 |||| | ||::|:||||: |::|::|:||||:||||:||||||| ||||| ||
 Db 416 LENC GTVALTIIRRGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

Qy 468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
 |||||:| | |||:: | |:|: | | | | |||| ||
 Db 476 IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVS---TLACLGSPSTATVTIFDDD 532

Qy 528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
 ||||| |||||:||||| ||||:|:||||:||||| ||
 Db 533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy 588 EFKNDETV 595
 ||:| | |
 Db 593 EFQNDEIV 600

RESULT 15

AAM13701

ID AAM13701 standard; protein; 609 AA.

XX

AC AAM13701;

XX

DT 12-OCT-2001 (first entry)

XX

DE Peptide #135 encoded by probe for measuring cervical gene expression.

XX

KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.

XX

OS Homo sapiens.

XX

PN WO200157278-A2.

XX

PD 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US000670.

XX

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

DR WPI; 2001-488901/53.

XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.

XX

PS Claim 27; SEQ ID NO 18527; 487pp; English.

Qy 588 EFKNDE 593
 ||:||||
Db 603 EFQNDE 608

Search completed: June 24, 2004, 16:11:58
Job time : 45.05 secs

OM protein - protein search, using sw model

Run on: June 24, 2004, 16:09:57 ; Search time 15.6911 Seconds
 (without alignments)
 2039.888 Million cell updates/sec

Title: US-10-054-680-4
 Perfect score: 3228
 Sequence: 1 MAWLRLQPLTSAFLHFGLVT.....ADYGRGGQEDSRDGKASIG 620

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	362.5	11.2	539	4	US-09-701-068-2	Sequence 2, Appli	
2	294.5	9.1	474	4	US-09-701-068-5	Sequence 5, Appli	
3	113.5	3.5	339	4	US-09-134-001C-3608	Sequence 3608, Ap	
4	108.5	3.4	652	1	US-08-050-684-2	Sequence 2, Appli	
5	108.5	3.4	652	1	US-08-582-719-2	Sequence 2, Appli	
6	106.5	3.3	501	4	US-09-489-039A-9817	Sequence 9817, Ap	
7	105	3.3	404	4	US-09-198-452A-718	Sequence 718, App	
8	103.5	3.2	988	2	US-08-286-819A-19	Sequence 19, Appl	
9	103.5	3.2	988	3	US-08-980-357-19	Sequence 19, Appl	
10	103	3.2	519	3	US-08-997-445D-2	Sequence 2, Appli	
11	100.5	3.1	330	4	US-09-134-001C-3811	Sequence 3811, Ap	

12	99.5	3.1	704	4	US-09-543-681A-7274	Sequence 7274, Ap
13	97.5	3.0	666	4	US-08-671-757A-13	Sequence 13, Appl
14	97.5	3.0	10182	4	US-09-134-001C-3159	Sequence 3159, Ap
15	96.5	3.0	429	4	US-09-107-532A-7193	Sequence 7193, Ap
16	94	2.9	583	4	US-09-328-352-6422	Sequence 6422, Ap
17	93	2.9	447	4	US-08-836-687B-39	Sequence 39, Appl
18	92.5	2.9	368	4	US-09-328-352-7684	Sequence 7684, Ap
19	92.5	2.9	1976	3	US-09-024-020B-9	Sequence 9, Appli
20	92.5	2.9	1976	4	US-09-425-043-9	Sequence 9, Appli
21	92.5	2.9	1978	3	US-09-024-020B-3	Sequence 3, Appli
22	92.5	2.9	1978	4	US-09-425-043-3	Sequence 3, Appli
23	92.5	2.9	1988	3	US-09-024-020B-4	Sequence 4, Appli
24	92.5	2.9	1988	4	US-09-425-043-4	Sequence 4, Appli
25	92	2.9	567	4	US-09-107-532A-6730	Sequence 6730, Ap
26	92	2.9	749	4	US-09-562-737-98	Sequence 98, Appl
27	92	2.9	911	4	US-09-489-039A-13537	Sequence 13537, A
28	91.5	2.8	382	4	US-09-252-991A-29696	Sequence 29696, A
29	91.5	2.8	503	4	US-09-562-737-67	Sequence 67, Appl
30	91.5	2.8	644	2	US-08-866-757-2	Sequence 2, Appli
31	91.5	2.8	644	3	US-09-153-593-2	Sequence 2, Appli
32	91	2.8	922	4	US-09-252-991A-32759	Sequence 32759, A
33	90.5	2.8	589	4	US-09-489-039A-12592	Sequence 12592, A
34	90.5	2.8	708	2	US-08-576-165-2	Sequence 2, Appli
35	90.5	2.8	1912	4	US-09-495-714C-2	Sequence 2, Appli
36	90.5	2.8	1977	4	US-09-495-714C-4	Sequence 4, Appli
37	90	2.8	497	3	US-09-058-947A-4	Sequence 4, Appli
38	90	2.8	500	4	US-08-868-373-12	Sequence 12, Appl
39	90	2.8	548	3	US-08-656-034-10	Sequence 10, Appl
40	90	2.8	594	4	US-09-107-532A-7250	Sequence 7250, Ap
41	90	2.8	612	4	US-09-252-991A-17516	Sequence 17516, A
42	90	2.8	628	3	US-08-656-034-2	Sequence 2, Appli
43	90	2.8	1003	4	US-09-198-452A-17	Sequence 17, Appl
44	89.5	2.8	1052	3	US-09-255-502-7	Sequence 7, Appli
45	89.5	2.8	1052	4	US-09-360-237-3	Sequence 3, Appli

ALIGNMENTS

```

RESULT 1
US-09-701-068-2
; Sequence 2, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

```

US-09-701-068-2

Query Match 11.2%; Score 362.5; DB 4; Length 539;
Best Local Similarity 31.3%; Pred. No. 3e-28;
Matches 91; Conservative 61; Mismatches 96; Indels 43; Gaps 9;

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Qy      64 YPENPSLGDKIARVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIKKPNGETST 123
      :|  :|  | :  | ::||:  |  | :||:|  |  ||  |:|  :  |:|  |  :
Db      29 FPGENTLSDGL-RGVLYFLGLAYCFIGLSAITARFFKSMENVVKHSRKVVTIDPITKAEV 87

Qy      124 TTI-RVWNETVSNLTLMALGSSAPEILLSLIEV---CGHGFIAGDLGPSTIVGSAAFNMF 179
      |  :||| |:::~::~|:| |:| |:| |:|  |  :  || ||| |:|||||::|
Db      88 ITYKKVWNFTIADISLLAFGTSEFPQISLATIDAIRNMGERY-AGGLGPGTLVGSAAFDLF 146

Qy      180 IIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLF 239
      |  :||  |  || :||  |  | :  |  | :|||~::~|:| |:| |:|  | |||:
Db      147 PIHAVCVVVPKAGELKKISDLGVWLVELVWSFWAYIWLYIILEVWSPNVITLVEALLTVL 206

Qy      240 FFPVCVLLAWVADKRLLFYKYMHHKRYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDG 299
      :  :  :  |:  |||  :  |:  :  :  :  :  :  :  :  :  :  :  :
Db      207 QYGLLLVHAYAQDKR---WPYLS-----LPMRGDRPE----- 236

Qy      300 NLVPLEGKEVDESR----REMIRILKDLKQKHPEKDLDQLVEMANYALSH 346
      ||  :|:| |:  :  :  :  |  |  |  :|:~::~:~::~:
Db      237 EWVP---EEIDTSKDDNDNDVDVYSDAAQDAVESGSRNIVDIFSISANN 284
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RESULT 2

US-09-701-068-5

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; Sequence 5, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-701-068-5
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Query Match 9.1%; Score 294.5; DB 4; Length 474;
Best Local Similarity 30.7%; Pred. No. 2.5e-21;
Matches 79; Conservative 52; Mismatches 73; Indels 53; Gaps 9;

```
Qy      97 RFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEV- 155
      |  :  :|: ||  |  :|  ||  ||| |:::~::~|:| |:| |:| |:|  |
Db      9  RKVVTIDPITKAE-VITYKK-----VWNFTIADISLLAFGTSEFPQISLATIDAI 56

Qy      156 --CGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFA 213
      |  :  || ||| |:|||||~::~|  |  :||  |  || :||  |  |:  :  ||  :|
```

```

Db          57 RNMGERY-AGGLPGGTLVGSAAFDLFPIHAVCVVVPKAGELKKISDLGVWLVELVWSFWA 115
Qy          214 YIWLYMILAVFSPGVVQVWEGLLTLFFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGI 273
          |||||:| | :| | : | ||| : : : :| : ||| : | :
Db          116 YIWLYIILEVWSPNVITLVEALLTVLQYGLLLVHAYAQDKR---WPYLS----- 161
Qy          274 IIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESR---REMIRILKDLKQKHPE 329
          : : || | : || :| :| | : : : | | |
Db          162 LPMSRGDRPE-----EWVP---EEIDTSKDDNDNDVHDVYSDAQAQDAVE 202
Qy          330 KDLDQLVEMANYYALSH 346
          :| : : : : :
Db          203 SGRNIVDIFSIHSANN 219

```

RESULT 3

US-09-134-001C-3608

; Sequence 3608, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3608

; LENGTH: 339

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3608

Query Match 3.5%; Score 113.5; DB 4; Length 339;

Best Local Similarity 20.4%; Pred. No. 0.0072;

Matches 69; Conservative 53; Mismatches 149; Indels 67; Gaps 12;

```

Qy          195 RKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFFPVCVLLAWVADKR 254
          |||| : | : : | | | : :| :|| | :| | | : : |
Db          3 RKIKRSDLMF-SIGFIIIAVIIVVALLILFSFVPVGLWISALAA---GVHVGIGTLVGMR 58
Qy          255 LLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFL-----DGNL----- 301
          | | | | | :| | | :| : : : ||:| | | :
Db          59 L-----RRVSPRKVIAPLIKAHKAGLNLTTNQLESHYLAGGNVDRVVDANIAAQR 108
Qy          302 ----VPLE-GKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRIFYRI 356
          :| | | :| : | : : : : : : : : : :| :|
Db          109 ADIDLPFERGAIDLGRDVLEAVQ--MSVNPKVIETPFIAGVAMNGIEVKAKARITVRA 166
Qy          357 QATRMMTGAG-NILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSQCLENCGAVL 415
          | : : ||| : | | | | | : ||| :
Db          167 NIARLVGGAGEETIARVGEIVSTIGSSEHHT-----EVLENPDNIS 209

```

Qy 416 LTVVRKG---GDMSKTMVVDYKTEDGSANAGADYE----FTEGTVVLKPGETQKEFSVGI 468
 ||: || | : : :| | | ||| : : : | : : |
 Db 210 KTVLSKGLDSGTAFEILSIDIADVDISKNIGADLQTEQALADKNIAQAKAEERRAMAVA- 268
 Qy 469 IDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSL 506
 :: | : : | : : | : | : | : |
 Db 269 -----SEQEMKARVQEMRAKVVEAESEVPLAMAEAL 299

RESULT 4

US-08-050-684-2

; Sequence 2, Application US/08050684
 ; Patent No. 5550221
 ; GENERAL INFORMATION:
 ; APPLICANT: Johann Dr., Stephen V.
 ; APPLICANT: Van Zeijl Dr., Marja
 ; APPLICANT: O'Hara Dr., Bryan M.
 ; TITLE OF INVENTION: Amphotropic Virus Receptor
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: American Cyanamid Company
 ; STREET: 1937 West Main Street
 ; CITY: Stamford
 ; STATE: CT
 ; COUNTRY: United States of America
 ; ZIP: 06904-0060
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/050,684
 ; FILING DATE: 16-APR-1993
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lowney Dr., Karen A
 ; REGISTRATION NUMBER: 31,274
 ; REFERENCE/DOCKET NUMBER: 31937-00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 203-321-2361
 ; TELEFAX: 203-321-2971
 ; TELEX: 710-474-4059
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 652 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-050-684-2

Query Match 3.4%; Score 108.5; DB 1; Length 652;
 Best Local Similarity 19.9%; Pred. No. 0.072;
 Matches 124; Conservative 89; Mismatches 210; Indels 201; Gaps 30;

Qy 77 VIVYFVALIYMF-LGVSIADRFMASI--EVITSQER-----EVTIKKPNGET- 121

```

      :: : : | | : | : : : | : : | : | : :
Db      11 ILGFIIAFILAFSVGANDVANSFGTAVGSGVVTLRQACILASIFETTGSVLLGAKVGETI 70

Qy      122 --STTTIRVWNETVSNLTLMA-----LGSSAPEILLSLIE--VCG-HGFIAGDLGPSTI 170
      : : : | | | | | : : : : : | : : : | : : :
Db      71 RKGIIIDVNLNETVE--TLMAGEVSAMVGSQVQLIASFLRLPISGTHCIVGSTIGFSLV 128

Qy      171 V-----GSAAFNMFIIGICVYVIPDGETRKHHLRVFF- 204
      | : : : : | : | : : | : | :
Db      129 AIGTKGVQWMELVKIVASWFIPLLSGFMSSGLLFVLIRIFILKKEDVPNGLRALPVFYA 188

Qy      205 ITAAWSIFAYIW-----LYMILAVFSPGVVQVWEGLLTLFFFVPCV----- 245
      | | : : : : : | : : : : : : | | : | :
Db      189 ATIAINVFSIMYTGAPVLGLVLPWMAIALISFGVALLFAFFVWLFVCPWMRRKITGKLQK 248

Qy      246 --LLAWVADKRL-----LFYKYMHHKKYRTDKH---RGIIEET-----EGDHPK 283
      | : | : : | : : : | : | : | : | : | :
Db      249 EGALSRVSDSLSKVQEAESPVFKELPGAKANDDSTIPLTGAAGETLGTSEGTSAGSHPR 308

Qy      284 GI-----EMDGKMMNSHF-----LDGNLVPLEGKEVDESRRMIRILKDLKQK 326
      : : : | | : : : | : : : : : : : | | |
Db      309 AAYGRALSMTHGSVKSPISNGTFGFDGHTRSDGHVYHTVHKDSG-----LYKDLLHK 360

Qy      327 -HPEKDLDQLVEMANYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSE 385
      | : : : : : | | : | | : | : | | : | :
Db      361 IHIDRGPEEKPAQESNYRLLRRNNSYTCY----TAAICG----LPVHATFRAADSSA--- 409

Qy      386 VHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGAD 445
      | | | | : | | | : | : : : | | | :
Db      410 -----PED-SEKLVGDTVSY-----KKRLRYDSYSSYCNAAVAEAE 444

Qy      446 YEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPA--IF 503
      | | | : | : : | | | | | : | : | : |
Db      445 IEAEEGGVEMK-----LASELADPDQPREDP-----AEEKEEKDAPEVHLLF 487

Qy      504 NSLPLPRAVLAS-----PCVATVTILDDDHAGIFTFECDT-----IHV 541
      : | : | | | | | | | | | | | : :
Db      488 HFLQVLTACFGSFAHGGNDVSNAIGPLVALWLIYKQ---GGVTQEATPVWLLFYGGVGI 544

Qy      542 SESIGVMEVKVLRITSGARGTVVIP 565
      : | : : : | | |
Db      545 CTGLWVWGRRVIQTMGKDITPITP 568

```

RESULT 5

US-08-582-719-2

; Sequence 2, Application US/08582719

; Patent No. 5633348

; GENERAL INFORMATION:

; APPLICANT: Johann Dr., Stephen V.

; APPLICANT: Van Zeijl Dr., Marja

; APPLICANT: O'Hara Dr., Bryan M.

; TITLE OF INVENTION: Amphotropic Virus Receptor

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: 1937 West Main Street


```

          :  : | |          ||::  :          : || | |
Db      309 AAYGRALSMTHGSKVSPISNGTFGFDGHTSDGHVYHTVHKDSG-----LYKDLLHK 360
Qy      327 -HPEKDLQLVEMANYALSHQQKSRFYRIQATRMMTGAGNILKKHAAEQAKKASSMSE 385
          | :: ::      : | | : | |      | : |      | | : | : | :
Db      361 IHIDRGPEEKPAQESNYRLLRRNNSYTCY----TAAICG----LPVHATFRAADSSA--- 409
Qy      386 VHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGAD 445
          || |      | : | ||          | : | : : | | | :
Db      410 -----PED-SEKLVGDTVSYSS-----KKRLRYDSYSSYCNAAVAEAE 444
Qy      446 YEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPA--IF 503
          | | | : |      : : | | ||          || | : | : | : |
Db      445 IEAEEGGVEMK-----LASELADPDQPREDP-----AEEKEEKDAPEVHLLF 487
Qy      504 NSLPLPRAVLAS-----PCVATVTILDDDHAGIFTFECDT-----IHV 541
          : | : | |      | | | | | | | | | | | | : :
Db      488 HFLQVLTACFGSFAHGGNDVSNAIGPLVALWLIYKQ---GGVTQEAATPVWLLFYGGVGI 544
Qy      542 SESIGVMEVKVLRTSGARGTVIVP 565
          : | : : | | | | |
Db      545 CTGLWVWGRRVIQTMGKDLTPITP 568

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RESULT 6

```

US-09-489-039A-9817
; Sequence 9817, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9817
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9817

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Query Match          3.3%; Score 106.5; DB 4; Length 501;
Best Local Similarity 19.8%; Pred. No. 0.074;
Matches 82; Conservative 66; Mismatches 156; Indels 111; Gaps 16;

```

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Qy      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120
          | | | | | | | | | | | | | | | | | | | | | | | |
Db      146 PDWLTCNP-----APVVNQNDAVIYYFRNIMMAVLFMSSIILYYFRQIMHSWKAHVL 199
Qy      121 TSTTTIRVWNETVSNLTLMAL----GSSAPEILLSLIEVCGHGFIAGDLGP--STIVGSA 174
          | | | : ||:: | | : | : : : | | | : | : |
Db      200 TFTACI-----LFTLTIIVLSWLYSSHSPWLSVNFIDDLSTFT-----PLWQSIIGWL 248

```

Qy 175 AFNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVW-- 232
 Db 249 LMAVWFITLILLISLS-----KLRNIFWFSGAFFCSAYLFTLFQLLSTAGELDQTWYQ 301
 Qy 233 -----EGLLTLEFFFPVCVLLAWVADKRLLF----YKYM-----KKYRTDK 269
 Db 302 ARFFETLCTLF-----LILVLLVDVFILYRESNHKYVHSYQNSIRDPLTRLNRSFFYDT 356
 Qy 270 HRGIIIEGTEGHPKGI---EMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQK 326
 Db 357 LNQQAKVNAQHPLSVLISDLD-----HF-----KRINDSYGHVAG----- 392
 Qy 327 HPEKDLDQLVEMANYALSHQQKSRIFYRI---QATRMGTGAGNILKKHAAEQAKKASSM 383
 Db 393 -----DKVIQFAASVLESHSRVDDAAARIGGEEFALLLVNTGEKEAQAIAERIRLAVSA 446
 Qy 384 SEVHTDEPEDFISKVF-----FDPCSYQCLENCGAVLLTVVRKGG 423
 Db 447 GESHLPERMTISMGVYTTDNSVTAEACVQRADEAMYEAKNNGRNQVIVWHRQGG 501

RESULT 7

US-09-198-452A-718

; Sequence 718, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 718

; LENGTH: 404

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-718

Query Match 3.3%; Score 105; DB 4; Length 404;

Best Local Similarity 21.5%; Pred. No. 0.073;

Matches 79; Conservative 51; Mismatches 154; Indels 84; Gaps 15;

Qy 265 YRTDKHRGIIIEGTEGHPKGIEMDGKMMNSHFLD-----GNLVPLEGKEVDESRRMIR 318
 Db 48 YLLKKHAAVILMSHLGRPKGQGFQEEYSLQPVDVLEGYLGHHVPLAPDCVGEVARQAVA 107
 Qy 319 -----ILKDLK----QKHPEKDLDQLVEMANY-----YALSHQQKSRIFYRIQA 358
 Db 108 QLSPGRVLLLENLRFHIGEEHPEKDPTFAAELSSYGDFYVNDAFGTSHRKHASVYVVPQA 167
 Qy 359 TRMTGTGAGNILKK-----HAAEQAKK-----ASSMSEVHTDEPEDFISKVFFDPC 403
 Db 168 FPGRAAAGLLMEKELEFLGRHLLTSPKRPFTAILGGAKISSKIG-----VIEALLNQV 220

Qy 404 SYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVL----KPGE 459
 | | | : | :: | | : | : | : | : | | |
 Db 221 DYLLL--AGGMGFTFLQALGKSLGNSLVEKSALDLARNVLKIAKSRNVTIVLPSDVKAAE 278
 Qy 460 T--QKEFSVGIIDD-----DIFEEDEHFFVRLSN-----VRIEEEQPEEGM 498
 ||:|| || || || || || :|| | : | :
 Db 279 NLQSKYSVISIDQGIPPHLQGFDIGPRTTEEFIRIINQSATVFWNGPVGVE-----V 332
 Qy 499 PPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDT--IHVSESIGVMEVKVLRIS 556
 || | : : | : | | | | : | | || | : : |
 Db 333 PPFDSGSIAIANALGNHPSAVTVVGGGDAAAVVALAGCSTKVSHVSTG--GGASLEFLEQG 391
 Qy 557 GARGTVIV 564
 || ::
 Db 392 FLPGTEVL 399

RESULT 8

US-08-286-819A-19

; Sequence 19, Application US/08286819A

; Patent No. 5871910

; GENERAL INFORMATION:

; APPLICANT: ARTHUR, MICHEL

; APPLICANT: DUKTA-MALEN, SYLVIE

; APPLICANT: MOLINAS, CATHERINE

; APPLICANT: COURVALIN, PATRICE

; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE

; TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN

PARTICULAR

; TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING
 FOR

; TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

; NUMBER OF SEQUENCES: 54

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. Jefferson Davis Highway, Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/286,819A

; FILING DATE: 05-AUG-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/174,682

; FILING DATE: 28-DEC-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/917,146

```

; FILING DATE: 10-AUG-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR/91/00855
; FILING DATE: 29-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9013579
; FILING DATE: 31-OCT-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5871910man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-060-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 988 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-819A-19

```

```

Query Match          3.2%; Score 103.5; DB 2; Length 988;
Best Local Similarity 19.3%; Pred. No. 0.48;
Matches 116; Conservative 89; Mismatches 173; Indels 223; Gaps 32;

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Qy      3 WLRLQPLTSAFLHFGLVTFVL-----FLNGLRAEAGGSGDVPSTGQNNESCSGSSDC 54
      | |::| : ||| | :|: | | |:: |
Db      104 WDHLKEIRS---EYDFVTFTLSEYRMTFKYLHQLALE-----NGDAIHLHLEC 148

Qy      55 -----KEGVILP-----IWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMAS 101
      | :||| :| | : :| :| ||
Db      149 IDFLRKNKIILPAITTLERMVW--EARAMAEK-----KLFNTVS----- 185

Qy      102 IEVITSQERE-----VTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVC 156
      : :|:::| :| :| : | || | : | :|| | :||
Db      186 -KSLTNEQKEKLEGIITSQHPS--ESNKTILGWLKEPP-----GHPSPETFLKIIE-- 233

Qy      157 GHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKKIKHL---RVFFITA----- 207
      : | |: | || :| || | : ::
Db      234 -----RLEYIRGM-----DLETVQISHLHRNRLQLSRLGSRYE 267

Qy      208 --AWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKY 265
      |: | | || :: :|: : | | : |: :| :|
Db      268 PYAFRDFQENKRYSIILTIY---LLQLTQELTDKAF-----EIHDRQILSLLSKGRKA 316

Qy      266 RTDKHRGIIIEGTHPKGIEMDGKMMNS---HFLDGNLVPLEGKEVDESRRMIRILKD 322
      : : : :||: | || : | : :| | : : |
Db      317 QEEIQK-----QNGKKLNEKVIHFTN-----IGQALIKAREEKLDVFKV 355

Qy      323 LKQ-----KHPEKDLDQLVEMANYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAE 375
      |: : :| | :| | || || : : :| :| :
Db      356 LESVIEWNTFVSSVEEAQELARPADYDYDLLQK--RFYSLR--KYTPTLRLRVLEFHSTK 411

```

Qy	376	-----QAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVL-----	415
		: : : : :	
Db	412	ANEPLLQAVEIIRGMNESGKRKVPDDSPVDFISKRW----KRHLYEDDGTGINRHHYEMA	467
Qy	416	-LTVVR---KGGDMS---KTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGI	468
		: : : :: : : : :	
Db	468	VLTELREHVRAGDVSIVGSRQYRDFE-----EYLFSEDTWNQSKGNTRLVSVLS-	516
Qy	469	IDDDIFEEDHEHFFVR-----LSNVRIEEEQPEEG--MPPAIFNSL	506
		: : : : :::	
Db	517	FEDYITERTSSFNERLKWLAANSNKLDGVSLEKGLSLARLEKDVPEEAKKFSASLYQML	576
Qy	507	P 507	
Db	577	P 577	

RESULT 9

US-08-980-357-19

; Sequence 19, Application US/08980357

; Patent No. 6013508

; GENERAL INFORMATION:

APPLICANT: ARTHUR, MICHEL

; APPLICANT: DUKTA-MALEN, SYLVIE

; APPLICANT: MOLINAS, CATHERINE

; APPLICANT: COURVALIN, PATRICE

7 TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE

10 TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN

PARTICULAR

10 TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING

FOR

7 TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

NUMBER OF SEQUENCES: 54

; CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. Jefferson Davis Highway, Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

ZIP: 22202

; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
```

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;      COMPUTER:  IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/08/980,357

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,819

FILING DATE: 05-AUG-1994

; APPLICATION NUMBER: US 08/174,682

FILING DATE: 28-DEC-1993

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/917,146

```

; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR/91/00855
; FILING DATE: 29-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9013579
; FILING DATE: 31-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 6013508man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-060-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 988 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-980-357-19

```

```

Query Match          3.2%; Score 103.5; DB 3; Length 988;
Best Local Similarity 19.3%; Pred. No. 0.48;
Matches 116; Conservative 89; Mismatches 173; Indels 223; Gaps 32;

```

```

Qy      3 WLRLQPLTSAFLHFGLVTFVL-----FLNGLRAEAGGSGDVPSTGQNNESCSGSSDC 54
      | | : : | : || | : | : | : | : | : | : | : | : | : | : | : |
Db     104 WDHLKEIRS---EYDFVTFTLSEYRMTFKYLHQLALE-----NGDAIHLLHEC 148

Qy      55 -----KEGVILP-----IWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMAS 101
      | : || | : | | : : : | : | | : | : | : | : | : | : | : |
Db     149 IDFLRKNKIILPAITTLERMVW--EARAMAEK-----KLFNTVS----- 185

Qy     102 IEVITSQERE-----VTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVC 156
      : : | : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     186 -KSLTNEQKEKLEGIITSQHPS--ESNKTILGWLKEPP-----GHPSPETFLKIIE-- 233

Qy     157 GHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRRIKHL---RVFFITA----- 207
      : | | : | | : | | : | : | : | : | : | : | : | : | : | : |
Db     234 -----RLEYIRGM-----DLETVQISHLHRNRLQLSRLGSRYE 267

Qy     208 --AWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKY 265
      | : | | | : : : : | : | : | : | : | : | : | : | : | : |
Db     268 PYAFRDFQENKRYSIILTIY---LLQLTQELTDKAF-----EIHDRQILSLLSKGRKA 316

Qy     266 RTDKHRGIIIETEGDHPKGIEMDGKMMNS---HFLDGNLVPLEGKEVDESRRMIRILKD 322
      : : : : : : | : | : | : | : | : | : | : | : | : | : | : |
Db     317 QEEIQK-----QNGKKLNEKVIHFTN-----IGQALIKAREEKLDVFKV 355

Qy     323 LKQ-----KHPEKDLDQLVEMANYALSHQQKSRAFYRIQATRMMTGAGNIIKKHAAE 375
      | : : : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     356 LESVIEWNTFVSSVEEAQELARPADYDLDLLQK--RFYSLR--KYTPTLRLRVLEFHSTK 411

Qy     376 -----QAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVL----- 415
      : | : | | | | : | : | : | : | : | : | : | : | : | : | : |

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Db 412 ANEPLLQAVEIIRGMNESGKRKVPDDSPVDFISKRW----KRHLYEDDGT TINRHYEMA 467
 Qy 416 -LTVVR---KGGDMS---KTMVVDYKTEDGSANAGADYEFTEGT VVLKPGETQKEFSVGI 468
 || :| : ||:| | |:: :| | :| | | : | :
 Db 468 VLTELREHVRAGDVSIVGSRQYRDFE-----EYLFSEDTWNQSKGNTRLSVSL- 516
 Qy 469 IDDDIFEDEHFFVR-----LSNVRIEEEQPEG--MPPAIFNSL 506
 :| | | | | | | | | | :| :| :| | | : : : |
 Db 517 FEDYITERTSSFNERLKWLAANSNKLDGVSLEK GKLSLARLEKDVPEEAKKFSASLYQML 576
 Qy 507 P 507
 |
 Db 577 P 577

RESULT 10

US-08-997-445D-2

; Sequence 2, Application US/08997445D

; Patent No. 6043342

; GENERAL INFORMATION:

; APPLICANT: Kocher, Olivier N.

; TITLE OF INVENTION: PDZK1 Protein Containing PDZ

; TITLE OF INVENTION: Interaction Domains

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David Prashker, Esq.

; STREET: P.O. Box 67

; CITY: Brookline

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02146

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage

; COMPUTER: IBM PS/1

; OPERATING SYSTEM: MS DOS

; SOFTWARE: WordPerfect version 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/997,445D

; FILING DATE: December 23, 1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: David Prashker

; REGISTRATION NUMBER: 29,693

; REFERENCE/DOCKET NUMBER: BIS-037

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 232-7509

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 519 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-997-445D-2

Query Match 3.2%; Score 103; DB 3; Length 519;

Best Local Similarity 20.7%; Pred. No. 0.18;

Matches 47; Conservative 44; Mismatches 90; Indels 46; Gaps 10;

Qy	282	PKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMI-----RIL-----KDLKQKH	327
Db	165	PQGVAMRAGVL----ADDHLIEVNGENVEDASHEKVVVEKVKKSGSRVMFLLVDKETDKRH	220
Qy	328	PEKDLQQLVEMANYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVH	387
Db	221	VEQKIQFKRETASLKLPHQPRI-----VEMKKGSNGYGFYLR--AGSEQKGQIIKDID	272
Qy	388	TDEP-----EDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGS	439
Db	273	SGSPAEEAGLKNNDLVVAVNGE--SVETLDHDSVV--EMIRKGGDQTSLLVVDKETDNMY	328
Qy	440	ANAG-----ADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDH	479
Db	329	LRAHFSPFLYYOSOELPNGSVKEAPAPTPTSLEVS-SPPDTTEEVDH	374

Qy	9	L TSAFLHFGLVTFVLFL---NGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYP	65
		: : : : :	
Db	116	L VVG FV VFSIVTIVQFLVITKGSERVAEVAARFSLDGM PGKQMSIDADLKSGII-----	169
Qy	66	ENPSL-----GDKIARVIVYFVALIYMFLGVSI IADRFMA	100
		: :: : :	
Db	170	TNEEVQIRRKELGQESQLYGSFDGAMKFIKGD A IAGIVII FVNLIG---GISVGMAQMGL	226
Qy	101	SIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALG----SSAPEILLSLIEVC	156
		: : : : : :	
Db	227	SI-----TEALHTYTLTIGDGLVAQIPALLISI----	255
Qy	157	GHGFIAGDLGPSTIVGSAAFNMFI IIGICVYVIPDGETR KIKHLRVFFITA AWSIFAYIW	216
		: : : : : : :	
Db	256	SAGFIVTRVG-----GENNNLGY-----SIMNELLAQDF	284
Qy	217	LYMILAV-----FSPG---VVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYM HKKYR	266
		: : : : : : : : : :	
Db	285	ALLV TAILAFGIGFLPGFP TPVFLILSVMLGVYFFKI---KWKSSK-----KEYK	331
Qy	267	TDKHRGII IETEGDHPKGI-----EMDGKMM--NSHFLDGNLVPL-----	304
		: : : : : : :	
Db	332	TEDEKDNHNATNADSKKGLMSNLFSGKHGEEVDNSLLTENITLSQAETLPLIITLSTKKK	391
Qy	305	-----EGKEVDESRRMIRILKDLKQK-----	326
		: : : : : : :	
Db	392	PYLTKIVFEKWLOKEFILOYGILLPDIVIHYS D KIDDDK---I I I I I N E V K A K E L N C P E P L	449

Qy 327 -HPEKDLQDLVEMA-----NYALSHQOKSRA-----FYR----- 355
 | | | : : : : : : : : : :
 Db 450 FHIEPNDELLSLGFNLISIEDDNKTHYWIERRDESKLAPLGykaERSESYFYRKFSDLI 509
 Qy 356 -----IQATRMGTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQ 406
 | | | : : : : : : : : : :
 Db 510 TLNITEFLGIQETKDIL---DKLEKSAPELLKEC--YRQVSIQRINDVLQRLVQEKIP-- 562
 Qy 407 CLENCGAVLLTVVRKGG-----DMSKTM---YVDY-KTEDGSANA---GADYE--- 447
 : | : : : : : : : : : : : : : :
 Db 563 -IRNIKTIIGGLVQWGSKEKDPVLLTEHIRTLLARYISYFFSTDGKFNAIILSNDMEEII 621
 Qy 448 -----FTEGTVV-LKPGETQKEF-SVGIIDDDIFEDEHFFVRLSNVR-----IEEEQ 493
 : | : : : : : : : : : : : : : :
 Db 622 RSGIRQSSSGTLLNLEPAELDMIIEKISMVIDDIKYIQDYIFLTSIDIRRFVKKLIETQY 681
 Qy 494 PE 495
 | :
 Db 682 PQ 683

RESULT 13

US-08-671-757A-13

; Sequence 13, Application US/08671757A

; Patent No. 6476213

; GENERAL INFORMATION:

; APPLICANT: Suerbaum, Sebastian

; TITLE OF INVENTION: Cloning and Characterization Production
 ; of Aflagellate Strains

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/671,757A

; FILING DATE: 16-Aug-2001

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 02356.0073-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:


```

;           LENGTH: 666 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;           MOLECULE TYPE: peptide
;           SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-671-757A-13

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Query Match           3.0%;  Score 97.5;  DB 4;  Length 666;
Best Local Similarity 20.8%;  Pred. No. 1;
Matches 128;  Conservative 83;  Mismatches 210;  Indels 193;  Gaps 33;

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Qy      9 LTS AFLH FGLVT---FVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYP 65
      |  | : | : ||  |::  |  | :  |  | : | | | : |
Db     91 LAVGFVIFSIVTVVQFIVITKGSERVAEVAARFSLDGMPGKQMSIDADLKAGIIDAAAGAK 150

Qy     66 ENPSL-----GDKIARVIVYFVALIYMFLGVSI IADRFMASIEVIT 106
      |  | :  |  | | | | : | | | |  | : | :  |  | :
Db    151 ERRSILERESQLYGSFDGAMKFIKGDAIAGIIIFVNLIG---GISVGMSQHGMSL---- 203

Qy    107 SQEREVTIKKPNGETSTTTTIRVWNETVSNLTL-MALGSSAPEILLSLIEVCGHGF----I 161
      : |  | | |  | | :  |  | | | : | : | :  |  | :
Db    204 -----SGALSTYTI-----LTIGDGLVSQIPALLISI----SAGFMLTRV 239

Qy    162 AGD---LGPSTIVGSAAFNMFIIGICVYVIPDGETR KIKHLRVFFITAAWSIFAYIWLY 218
      ||  : |  | :  | | : |  |  | : | :  |  | :
Db    240 NGDSDNMG-RNIMSQIFGNPFVLI-----VTSA----- 266

Qy    219 MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIE TE 278
      : || :  | : |  | | | | : | |  | : | | :  | : :
Db    267 LALAI-----GMLPGFPFFVFFLIA-VTLTALFYKKV-----VEKEKSLSSESDS 310

Qy    279 GDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMI-RILKDLKQKHPEKDLDQLVE 337
      :  : : |  | : |  | : |  | : |  | : |  | : | : | : |
Db    311 SGYTGTFDID-----NTH--DSSLAMIE--NLDRISETVPLILLFAENKINANDMEGLIE 362

Qy    338 MANYYALSHQOKSRAF--YRIQATRM MTGAGN ILKKHAAEQAKKASSMSEVHTDEPEDFI 395
      : : | : |  | : :  |  |  |  |  |  | : | | |  | :
Db    363 -----RIRSQFFIDYGVRLPTILYRTSNELKVDDI-----VLLINEVRADSFNIYF 408

Qy    396 SKVFFDPCSYQCL--EN--CGAVLLTVVRKGGDMSKTM YVDYKTEDGSANAGADYEFTEG 451
      ||  | :  | |  | : : | |  :  : | |  :  |  | :  :
Db    409 DKV-----CITDENG DIDALGIPV VSTSYNERVISWVDVSYTENLTNIDAKIKSAQ- 459

Qy    452 TVVLKPGETQKEFSVGIIID--DDIF-----EED E HFFV-RLSNV 487
      |  : |  : :  : : |  |  |  |  |  | : | : | |
Db    460 -----DEFYHQLSQALLNNINEIFGIQETKNMLDQFENRYPDLLKEVFRHV TIQRISEV 513

Qy    488 --RIEEEQPEEGMPPAIFNSLPL--PRAVLASPCVATVTILDDDHAGIFTFECDTIHVSE 543
      | :  |  |  | | | |  |  |  | : : :  | :  : |  | |
Db    514 LQRL LGENISVRNLKLIMESLALWAPRE-----KDVITLVEHV RASLSRYICS KIAVSG 567

Qy    544 SIGVMEVKVLR TSG 557
      | : | :  | |
Db    568 -----EIKVVMLSG 576

```

RESULT 14

US-09-134-001C-3159

; Sequence 3159, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3159

; LENGTH: 10182

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3159

Query Match 3.0%; Score 97.5; DB 4; Length 10182;

Best Local Similarity 21.5%; Pred. No. 1e+02;

Matches 73; Conservative 56; Mismatches 133; Indels 77; Gaps 16;

```

Qy      310 DESRREMIRILKDLKQ---KHPEKD-----LDQLVEMANYYA-----LSHQQK 349
          | : ::: || | :| |          :|| || |: ||::|
Db      9479 DATSNDLVNQAKDEGQSAIEHHADELPAKLDANQMIDQKVEDINHLISQNPNLNNEEK 9538

Qy      350 SRAFYRIQATRMMTGAGN----ILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSY 405
          :: :| ::: | | : | | | : : || : | :| :
Db      9539 NKLISQI--NKLVNGIKNEIQQAINKQIENA--TTKLDEVIETTKKLIIAKAE----AK 9590

Qy      406 QCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFS 465
          | ::          : | : | | :| || : || | |
Db      9591 QMIKELSQKKRDAINNNTDL-----TPSQKAHALADIDKTE-----KDALQHIENS 9636

Qy      466 VGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFN--SLPLPRAVLASPCVA---- 519
          | ||| || | |::: | : : | :| | | | :| |
Db      9637 NSI--DDINNKEHAFNTLAHIIIWDTDQQ----PLVFEVPELSLQNALVTSEVVHRDE 9690

Qy      520 -----TVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVE 570
          :: |: | : :| |:: : :|||: |: || || : ||
Db      9691 TISLESIKKMTLTDELKVNIVSLP-NTDKVADHL-TAKVKVILADGSYVTNVVPVKVVE 9748

Qy      571 GTAKGGGEDFEDTYG-----ELEFKNDETVCDRQEA 601
          : :| | ::: |: | |::|
Db      9749 KELQIAKKDAIKTIDVLVKQKIKDIDSNNELTSTQREDA 9787

```

RESULT 15

US-09-107-532A-7193

; Sequence 7193, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

```

;      APPLICANT: Lynn A Doucette-Stamm  and David Bush
;      TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                          ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND
THERAPEUTICS
;      NUMBER OF SEQUENCES: 7310
;      CORRESPONDENCE ADDRESS:
;          ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;          STREET: 100 Beaver Street
;          CITY: Waltham
;          STATE: Massachusetts
;          COUNTRY: USA
;          ZIP: 02354
;      COMPUTER READABLE FORM:
;          MEDIUM TYPE: CD/ROM ISO9660
;          COMPUTER: PC
;          OPERATING SYSTEM: <Unknown>
;          SOFTWARE: ASCII
;      CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/107,532A
;          FILING DATE: 30-Jun-1998
;      PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 60/085,598
;          FILING DATE: 14 May 1998
;          APPLICATION NUMBER: 60/051571
;          FILING DATE: July 2, 1997
;      ATTORNEY/AGENT INFORMATION:
;          NAME: Ariniello, Pamela Deneke
;          REGISTRATION NUMBER: 40,489
;          REFERENCE/DOCKET NUMBER: GTC-012
;      TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (781)893-5007
;          TELEFAX: (781)893-8277
;      INFORMATION FOR SEQ ID NO: 7193:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 429 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          HYPOTHETICAL: YES
;          ORIGINAL SOURCE:
;              ORGANISM: Enterococcus faecium
;          FEATURE:
;              NAME/KEY: misc_feature
;              LOCATION: (B) LOCATION 1...429
;          SEQUENCE DESCRIPTION: SEQ ID NO: 7193:
US-09-107-532A-7193

```

```

Query Match          3.0%;  Score 96.5;  DB 4;  Length 429;
Best Local Similarity 19.8%;  Pred. No. 0.61;
Matches   86;  Conservative   67;  Mismatches 158;  Indels 123;  Gaps   20;

```

```

Qy      107 SQEREVTIKKPNGETSTTTIRVW----NETVSNLTLMALGSSAPEILLSLIEVCGHGFIA 162
      | :: : | | : | : | | : : : : | : | : : |
Db      40 SNKQSIVAVSPTG-SGKTLAYLWPLLLNVEPGEASALVIFASSQELAIQVADVAREWGKD 98

Qy      163 GDLGPSTIVGSAAFNMFIIGICVYVIPDGETRRIKHL-----RVFFITAAWSIFAYIWL 217
      : | : : | | | | : | : | : | : | : | : | :

```


OM protein - protein search, using sw model

Run on: June 24, 2004, 16:07:32 ; Search time 14.0818 Seconds
(without alignments)
4235.175 Million cell updates/sec

Title: US-10-054-680-4
Perfect score: 3228
Sequence: 1 MAWLRLQPLTSAFLHFGGLVT.....ADYGRRGGQEDSRDGKASIG 620

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2159.5	66.9	970	2	A36417	Na+/Ca2+-exchangin
2	2147.5	66.5	970	2	S27114	Na+/Ca2+-exchangin
3	2146.5	66.5	973	2	S32815	Na+/Ca2+-exchangin
4	2142.5	66.4	970	2	I48097	Na+/Ca2+-exchangin
5	2138	66.2	957	2	A53789	Na+/Ca2+-exchangin
6	2136.5	66.2	941	2	B53335	Na+/Ca2+-exchangin
7	2135.5	66.2	935	2	S43730	Na+/Ca2+-exchangin
8	2135.5	66.2	958	2	S32435	Na+/Ca2+-exchangin
9	2129.5	66.0	971	2	S28833	Na+/Ca2+-exchangin
10	1954.5	60.5	921	2	A54139	Na+/Ca2+-exchangin
11	1196.5	37.1	890	2	B89047	protein C10G8.5 [i
12	633.5	19.6	807	2	T24110	hypothetical prote
13	362.5	11.2	538	2	T00424	probable Na+/Ca2+

14	205	6.4	1014	2	T31433	Na+/Ca2+,K+-exchan
15	198.5	6.1	1199	2	S20969	Na+/Ca2+,K+-exchan
16	187	5.8	4936	2	AH2515	hypothetical prote
17	178.5	5.5	591	2	T19746	hypothetical prote
18	170	5.3	611	2	T21747	hypothetical prote
19	169.5	5.3	3016	2	S77300	hypothetical prote
20	166	5.1	1568	2	T08616	aggregation factor
21	156.5	4.8	2205	2	T08615	aggregation factor
22	150.5	4.7	591	2	S40705	Na+/Ca2+,K+-exchan
23	144.5	4.5	703	2	T03888	Na+/Ca2+,K+-exchan
24	144	4.5	644	2	B96582	hypothetical prote
25	144	4.5	1428	2	AC2224	hypothetical prote
26	132	4.1	1807	2	JC6319	integrin beta-4 ch
27	131.5	4.1	826	2	AB1841	hypothetical prote
28	131	4.1	590	2	S40707	hypothetical prote
29	126.5	3.9	1875	2	A36429	integrin beta-4 ch
30	126	3.9	4199	2	S76412	hypothetical prote
31	124	3.8	318	2	A83708	hypothetical prote
32	122	3.8	825	2	T08617	aggregation factor
33	121.5	3.8	651	2	T03889	Na+/Ca2+,K+-exchan
34	121.5	3.8	743	2	T38674	probable membrane
35	119.5	3.7	433	2	S74922	hypothetical prote
36	119	3.7	3972	2	S75251	hypothetical prote
37	115	3.6	324	2	AI0434	probable sodium/ca
38	114	3.5	1748	1	JN0786	integrin beta-4 ch
39	113	3.5	332	2	H82064	conserved hypothet
40	112.5	3.5	375	2	I40554	rap60 protein - Ba
41	110	3.4	2397	1	A55535	versican precursor
42	109	3.4	769	2	G95270	hypothetical prote
43	108.5	3.4	652	2	A37000	leukemia virus rec
44	108	3.3	673	1	VCPVB5	coat protein VP1 -
45	107.5	3.3	1263	2	T00649	hypothetical prote

ALIGNMENTS

RESULT 1

A36417

Na+/Ca2+-exchanging protein - dog

C;Species: Canis lupus familiaris (dog)

C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 18-Aug-2000

C;Accession: A36417

R;Nicoll, D.A.; Longoni, S.; Philipson, K.D.

Science 250, 562-565, 1990

A;Title: Molecular cloning and functional expression of the cardiac sarcolemmal Na(+)-Ca(2+) exchanger.

A;Reference number: A36417; MUID:91047958; PMID:1700476

A;Accession: A36417

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-970 <NIC>

A;Cross-references: GB:M57523; NID:g164072; PIDN:AAA62766.1; PID:g164073;

GB:M36119

C;Superfamily: human Na+/Ca2+-exchanging protein

C;Keywords: phosphoprotein; transmembrane protein

Query Match 66.9%; Score 2159.5; DB 2; Length 970;
 Best Local Similarity 69.9%; Pred. No. 2.8e-157;
 Matches 425; Conservative 73; Mismatches 89; Indels 21; Gaps 8;

```

Qy      1 MAWLRLQPLTSAFLHFGLVTFVLF--LNLRLAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
      | ||| | | | | | :|| :: : || | : || : || ||: ||
Db      1 MLQLRLLPTFSMGCHLLAVVALLFSHVDLISAETEMEGERNETGE----CTGSYYCKKGV 56

Qy      59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN 118
      ||||| |: : || ||||| |||||: : ||||| |||||: ||||| |||||
Db      57 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPN 116

Qy     119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNM 178
      |||: ||: |: ||||| ||||| |||||: ||||| | ||||| |||||
Db     117 GETTKTTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 176

Qy     179 FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL 238
      |||| : ||||: ||||| ||||| ||||| ||||| ||||: |||||
Db     177 FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF 236

Qy     239 FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRIIETEGDHPKG---IEMDGKMMNSH 295
      ||||: ||: ||||: ||||| : : || | ||: || || | ||||: |||
Db     237 FFFPICVVFVAVADRRLLFYKYVYKRYRAGKQRMIIIEHGEDRPSSKTEIEMDGKVVNSH 296

Qy     296 ---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 348
      |||| || || | | | : |||| ||||: ||||| : : ||: || || ||
Db     297 VDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355

Qy     349 KSRAFYRIQATRMMTGAGNLIKKAHAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
      ||||| |||||: ||||| : ||: ||: || || ||: : | | : ||: ||: : |||
Db     356 KSRAFYRIQATRLMTGAGNLIKRAHADQARKAVSMHEVNTEVAENDPVSKIFFEQGTYQC 415

Qy     408 LENC GAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGT VVLKPGETQKEFSVG 467
      |||| | ||: |: ||: : ||: ||: ||||: ||||: ||||| ||||| ||
Db     416 LENC GTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGT VVFKPGETQKEIRVG 475

Qy     468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPAIFNSLPLPRAVLASPCVATVTILDDD 527
      ||||| ||||: | ||||: | ||: | | | || || || || || || ||
Db     476 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---ALACLGSPSTATVTIFDDD 532

Qy     528 HAGIFTFECDTIHVSESIGVMEVKVLRRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
      ||||| |||||: ||||| ||||| ||||: |: ||||: ||||| |||
Db     533 HAGIFTFEPPVTHVSESIGIMEVKVLRRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy     588 EFKNDETV 595
      ||: ||| |
Db     593 EFQNDIV 600

```

RESULT 2

S27114

Na⁺/Ca²⁺-exchanging protein precursor, cardiac - bovine

N;Alternate names: Na⁺/Ca²⁺ antiporter

C;Species: Bos primigenius taurus (cattle)

C;Date: 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 18-Aug-2000

C;Accession: S27114; S18388

R;Aceto, J.F.; Condrescu, M.; Kroupis, C.; Nelson, H.; Nelson, N.; Nicoll, D.; Philipson, K.D.; Reeves, J.P.
Arch. Biochem. Biophys. 298, 553-560, 1992
A;Title: Cloning and expression of the bovine cardiac sodium-calcium exchanger.
A;Reference number: S27114; MUID:93037494; PMID:1416984
A;Accession: S27114
A;Molecule type: mRNA
A;Residues: 1-970 <ACE>
A;Cross-references: GB:L06438; NID:g163033; PIDN:AAA30509.1; PID:g163034
R;Durkin, J.T.; Ahrens, D.C.; Pan, Y.C.E.; Reeves, J.P.
Arch. Biochem. Biophys. 290, 369-375, 1991
A;Title: Purification and amino-terminal sequence of the bovine cardiac sodium-calcium exchanger: evidence for the presence of a signal sequence.
A;Reference number: S18388; MUID:92027750; PMID:1929404
A;Accession: S18388
A;Molecule type: protein
A;Residues: 33-40,'X',42-44 <DUR>
A;Experimental source: heart
C;Superfamily: human Na⁺/Ca²⁺-exchanging protein
C;Keywords: cardiac muscle; heart; ion transport; membrane protein
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-970/Product: Na⁺/Ca²⁺ exchange protein, cardiac #status predicted <MAT>

Query Match 66.5%; Score 2147.5; DB 2; Length 970;
Best Local Similarity 69.4%; Pred. No. 2.4e-156;
Matches 422; Conservative 74; Mismatches 91; Indels 21; Gaps 8;

```

Qy      1 MAWLRLQPLTSAFLHFGVLTVFLV--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      1 MLQFSLSPTLSMGFHVIAVALLFSHVHDHISAETEMEGEGNETGE----CTGSYYCKKGV 56

Qy      59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN 118
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      57 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPN 116

Qy     119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAAFNM 178
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     117 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAAFNM 176

Qy     179 FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLMLAVFSPGVVQWEGLLTL 238
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     177 FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTF 236

Qy     239 FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH 295
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     237 FFFPICVVFVAVADRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPSSKTEIEMDGKVNSH 296

Qy     296 ---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLQLVEMANYALSHQQ 348
      ||| || || || || || :||| :||| :||| :||| :||| :||| :|||
Db     297 VDSFLDGALV-LEVDERDQDDEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355

Qy     349 KSRAFYRIQATRMMTGAGNILLKHAEEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     356 KSRAFYRIQATRLMTGAGNILLKHAADQARKAVSMHEVNTVAENDPVSKIFFEQGTYQC 415

Qy     408 LENCNAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
      ||||| | ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```


Db	416	LENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG	475
Qy	468	IIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD	527
		: :: : :	
Db	476	IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVS--TLACLGSPSTATVTIFDDD	532
Qy	528	HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL	587
		: :: : : : : :	
Db	533	HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL	592
Qy	588	EFKNETV	595
		:	
Db	593	EFONDEIV	600

Query Match 66.5%; Score 2146.5; DB 2; Length 973;
Best Local Similarity 69.2%; Pred. No. 2.8e-156;
Matches 421; Conservative 76; Mismatches 90; Indels 21; Gaps 8;

Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNM	178
Db	120	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM	179
Qy	179	FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL	238
Db	180	FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF	239
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKHGGIIETEGDHPKG---IEMDGKMMNSH	295
Db	240	FFFPICVVFVAVVADRRLLFYKYVYKRYRAGKQGRGMIIEHEGDRPSSKTEIEMDGKVVNSH	299
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQLVEMANYYALSHQQ	348
Db	300	VENFLDGLALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLSQQQ	358
Qy	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC	407
Db	359	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVTENDPVSKIFFEQGTYYQC	418
Qy	408	LENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
Db	419	LENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGDTQKEIRVG	478
Qy	468	IIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD	527
Db	479	IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD	535
Qy	528	HAGIFTFECDTIHVSESIGVMEVKVLRRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGEL	587
Db	536	HAGIFTFEEPVTHVSESIGIMEVKVLRRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL	595
Qy	588	EFKNDETV	595
Db	596	EFONDEIV	603

Query Match 66.4%; Score 2142.5; DB 2; Length 970;
Best Local Similarity 69.1%; Pred. No. 5.7e-156;

Matches 420; Conservative 76; Mismatches 91; Indels 21; Gaps 9;

```

Qy      1 MAWLRLQPLTSAFLH-FGLVTFVL-FLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MLRLSLSPYSLGFLHLLAMMTLLISHVDHITAET----EMVEEGNETGECTGSYYCKKGV 56

Qy      59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN 118
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      57 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPN 116

Qy     119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM 178
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     117 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 176

Qy     179 FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL 238
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     177 FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF 236

Qy     239 FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHGGIIETEGDHPKG---IEMDGKMMNSH 295
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     237 FFFPICVFAWVADRRLLFYKYVYKRYRAGKQRMIIIEHEDRPSKTEIEMDGKVVNSH 296

Qy     296 ---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLQLVEMANYALSHQQ 348
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     297 VENFLDGALV-LEVDERDQDDEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355

Qy     349 KSRAFYRIQATRMGTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     356 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTVAENDPVSKIFFEQGTYQC 415

Qy     408 LENCNAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     416 LENCGTVALTIIRGGDLTNTVFDVFRTEGDTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

Qy     468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPAIFNSLPLPRAVLASPCVATVTILDDD 527
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     476 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHIS---TLACLGSPSTATVTIFDDD 532

Qy     528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy     588 EFKNDETV 595
      | | | | |
Db     593 EFQNDIV 600

```

RESULT 5

A53789

Na⁺/Ca²⁺-exchanging protein precursor, splice form NACA7 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 18-Aug-2000

C;Accession: A53789; JX0288

R;Lee, S.L.; Yu, A.S.L.; Lytton, J.

J. Biol. Chem. 269, 14849-14852, 1994

A;Title: Tissue-specific expression of Na⁽⁺⁾-Ca⁽²⁺⁾ exchanger isoforms.

A;Reference number: A53789; MUID:94253030; PMID:8195112

A;Accession: A53789
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-957 <LEE>
 A;Cross-references: GB:U04933; NID:g451571; PIDN:AAB39952.1; PID:g451572
 R;Nakasaki, Y.; Iwamoto, T.; Hanada, H.; Imagawa, T.; Shigekawa, M.
 J. Biochem. 114, 528-534, 1993
 A;Title: Cloning of the rat aortic smooth muscle Na⁺/Ca²⁺ exchanger and tissue-specific expression of isoforms.
 A;Reference number: JX0288; MUID:94103175; PMID:8276763
 A;Accession: JX0288
 A;Molecule type: mRNA
 A;Residues: 1-957 <NAK>
 A;Experimental source: aortic smooth muscle
 C;Superfamily: human Na⁺/Ca²⁺-exchanging protein
 C;Keywords: ion transport; membrane protein
 F;1-32/Domain: signal sequence #status predicted <SIG>
 F;33-957/Product: Na⁺/Ca²⁺ exchanger #status predicted <MAT>

Query Match 66.2%; Score 2138; DB 2; Length 957;
 Best Local Similarity 67.9%; Pred. No. 1.2e-155;
 Matches 424; Conservative 73; Mismatches 87; Indels 40; Gaps 10;

Qy	4	LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK	55
		: : : :	
Db	2	LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK	53
Qy	56	EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK	115
		: :: :: : ::	
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK	113
Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAA	175
		: : :	
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL	235
		: : :	
Db	174	FNMFIIIALCVYVVPDGETRGIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL	233
Qy	236	LTLFFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMM	292
		: : : : : : : : :	
Db	234	LTFPPFPICVFAWVADRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPASKTEIEMDGKVV	293
Qy	293	NSH---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYALS	345
		: : : : :	
Db	294	NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qy	346	HQQKSRAFYRIQATRMGTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
		: : : : : :	
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSQVFFEQGT	412
Qy	405	YQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
		:: :: : :: : : : :	
Db	413	YQCLENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qy	465	SVGIIDDDIFEEDHEFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
		: : : : : :	

Qy	4	LRLQPLTSAFLHFLGLVTFVLFL-----NGLRAEAGSGDVPSTGQNNESCSCSSDCK	55
		: : :	
Db	2	LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK	53
Qy	56	EGVILPIWYPENPSLGDKIDRVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK	115
		: : : : : : : : :	
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK	113
Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA	175
		: : : :	
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL	235
		: : : : : :	
Db	174	FNMFIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL	233
Qy	236	LTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIIETEGDHPKG---IEMDGKMM	292

```

      || ||||:|: ||||:|||||:|:| || ||:| || || |||||:
Db      234 LTFFFFPICVFAWVADRRLLFYKYVYKRYRAGKQKGMIEHEGDRPASKTEIEMDGKV 293
Qy      293 NSH---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALS 345
      ||| |||| || || | | | :||| ||||:|||||:|:|:|:| ||
Db      294 NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS 352
Qy      346 HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
      ||||| |||||:|||||:|:|:|:| || ||: | | | :|||: |
Db      353 QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412
Qy      405 YQCLENCGAVLLTVVRKGGMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
      ||||| || | ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      413 YQCLENCGTVALTIIRRGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472
Qy      465 SVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
      ||||| |||||:| | ||||: | |:| | | : | | || ||:|
Db      473 RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528
Qy      524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
      ||||| ||||| |||||:||||| ||||| ||:|:|:|:|:|:|
Db      529 FDDDHAGIFTFEPEVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588
Qy      584 YGELEFKNDETV 595
      ||||:| || |
Db      589 CGELEFQNDIV 600

```

RESULT 8

S32435

Na⁺/Ca²⁺-exchanging protein RBE-2 - rat

N;Alternate names: Na⁺/Ca²⁺ antiporter; sodium-calcium exchanger RBE-2

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Aug-2000

C;Accession: S32435

R;Furman, I.; Cook, O.; Kasir, J.; Rahamimoff, H.

FEBS Lett. 319, 105-109, 1993

A;Title: Cloning of two isoforms of the rat brain Na⁽⁺⁾-Ca⁽²⁺⁾ exchanger gene and their functional expression in HeLa cells.

A;Reference number: S32435; MUID:93202244; PMID:8454039

A;Accession: S32435

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-958 <FUR>

A;Cross-references: EMBL:X68813; NID:g288231; PIDN:CAA48708.1; PID:g288232

C;Superfamily: human Na⁺/Ca²⁺-exchanging protein

```

Query Match          66.2%;  Score 2135.5;  DB 2;  Length 958;
Best Local Similarity 68.8%;  Pred. No. 1.9e-155;
Matches 421;  Conservative 72;  Mismatches 86;  Indels 33;  Gaps 9;

```

```

Qy      4 LRLQPLTSAFLHFGVLTVFLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK 55
      ||| : | ||| | | || ||: || || |
Db      2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53
Qy      56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIK 115
      :||||| |:| ||||| |||||:||||| |||||:|||||:|:|

```

Db 54 KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIK 113
 Qy 116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA 175
 |||||: ||:|:|||||||||||||||||||||:||||| | |||||||||||||
 Db 114 KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA 173
 Qy 176 FNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL 235
 ||||| :|||:|||||||||||||||||:||||||| ||:|:| ||||:|||||
 Db 174 FNMFIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL 233
 Qy 236 LTLFFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTDHPKG---IEMDGKMM 292
 || ||||:|:| ||||:|||||||:|:| || | ||:| || | |||||:|
 Db 234 LTLFFFFPICVFAWVADRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPASKTEIEMDGKVV 293
 Qy 293 NSH---FLDGNLVPLEGKEVD-----ESRREMIRILKDLKQKHPEKDLDQLVEMANYALS 345
 ||| |||| || || | | | :||| ||||:|||||:|:|:|:|:| || ||
 Db 294 NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS 352
 Qy 346 HQQKSRAFYRIQATRMGTAGNIIKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
 |||||||||||||:|||||||:|:|:|:| || ||:| | | :|||: |
 Db 353 QQQKSRAFYRIQATRLMTGAGNIIKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412
 Qy 405 YQCLENCGAVLLTVVRKGGMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
 ||||||| | ||:|:|:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 413 YQCLENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472
 Qy 465 SVGIIDDDIFEEDHFFVRLSNVRIEEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
 |||||||||||||:| | ||||: | :| | : | | || ||:|
 Db 473 RVGIIDDDIFEEDENFLVHLSNVRSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528
 Qy 524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
 ||||||||| |||||:||||||||||| ||:|:|:|:|:|:|:|
 Db 529 FDDDHAGIFTFEEPVTHSVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588
 Qy 584 YGELEFKNDETV 595
 |||||:||| |
 Db 589 CGELEFQNDIV 600

RESULT 9

S28833

Na⁺/Ca²⁺-exchanging protein - rat

N;Alternate names: Na⁺/Ca²⁺ antiporter; Na⁺/Ca²⁺ exchanger

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000

C;Accession: S28833; S25552

R;Low, W.; Kasir, J.; Rahamimoff, H.

FEBS Lett. 316, 63-67, 1993

A;Title: Cloning of the rat heart Na⁽⁺⁾-Ca⁽²⁺⁾ exchanger and its functional expression in HeLa cells.

A;Reference number: S28833; MUID:93138118; PMID:8422940

A;Accession: S28833

A;Molecule type: mRNA

A;Residues: 1-971 <LOW>

A;Cross-references: EMBL:X68191; NID:g57208; PIDN:CAA48273.1; PID:g57209

R;Low, W.; Kasir, J.; Boulter, J.; Heinemann, S.; Rahamimoff, H.
submitted to the EMBL Data Library, August 1992

A;Reference number: S25552
 A;Accession: S25552
 A;Molecule type: mRNA
 A;Residues: 1-194,'F',196-971 <LO2>
 A;Cross-references: EMBL:X68191
 C;Superfamily: human Na⁺/Ca²⁺-exchanging protein
 C;Keywords: ion transport; membrane protein; phosphoprotein

Query Match 66.0%; Score 2129.5; DB 2; Length 971;
 Best Local Similarity 68.6%; Pred. No. 5.7e-155;
 Matches 420; Conservative 72; Mismatches 87; Indels 33; Gaps 9;

Qy	4	LRLQPLTSAFLHFGVLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK	55
		: : :	
Db	2	LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK	53
Qy	56	EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK	115
		: : : : :	
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK	113
Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA	175
		: : : :	
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIIGICVYVIPDGETRKHKLRLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL	235
		: : : : : :	
Db	174	FNMFIIIALCVYVVPDGETRKHKLRLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL	233
Qy	236	LTLFFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMM	292
		: : : : : : :	
Db	234	LTLFFFFPICVFAWVAARLLFYKYVYKRYRAGKQGRMIIEHEGDRPASKTEIEMDGKVV	293
Qy	293	NSH---FLDGNLVPLEGKEVD-----ESRREMIRILKDLKQKHPEKDLDQLVEMANYALS	345
		: : : : : :	
Db	294	NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qy	346	HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
		: : : : : : : :	
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDAVSKVFFEQGT	412
Qy	405	YQCLENCGAVLLTVVRKGGMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
		: : : : : : : : : : : : : : :	
Db	413	YQCLENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qy	465	SVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
		: : : : :	
Db	473	RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG----ILDSNHVSAIACLGSPNTATITI	528
Qy	524	LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT	583
		: : : : : : :	
Db	529	FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGGEDFEDT	588
Qy	584	YGELEFKNDETV	595
		:	
Db	589	CGELEFQNDIV	600

A54139

Query Match 60.5%; Score 1954.5; DB 2; Length 921;
Best Local Similarity 64.1%; Pred. No. 1.4e-141;
Matches 371; Conservative 92; Mismatches 91; Indels 25; Gaps 6;

Qy	31	EAGSGDVPSTGQNN-----SCSGSSDCKEGLPIWIYPENPSLGDKIARVIVYFVALI	85
Db	21	EATPTPSLPPPPANDSDASPGGCQGSYRCQPGVLLPVWEPDDPSLGDKAARAVVYFVAMV	80
Qy	86	YMFLGVSIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSA	145
Db	81	YMFLGLSIIADRFMASIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSA	140
Qy	146	PEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRRIKHLRVFFI	205
Db	141	PEILLSVIEVCGHNFQAGELGPGTIVGSAAFNMFVVIACVYVIPAGESRKIKHLRVFFV	200
Qy	206	TAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFVPCVLLAWVADKRLLFYKYMHHKY	265
Db	201	TASWSIFAYVWLYLILAVFSPGVVQVWEALLTLVFFVPCVVFAMVADKRLLFYKYVYKRY	260
Qy	266	RTDKHRGIIIEGEGDHPKGIEMDGKMMNSHFLDGNL-----VPLEGKEVDESRRMIRIL	320
Db	261	RTDPRSGIIIGAEGDPPKSIELDGTFVGTE-VPGELGALGTGPAEARELDASRREVIQIL	319
Qy	321	KDLKQKHPEKDLQVLVEMANYYYALSHQQKSRAFYRIQATRMGTAGNIIKKHAAEQAKKA	380
Db	320	KDLKQKHPPDKDLEQLVGIKAKYYALLHQQKSRAFYRIQATRLMTAGNVLRRHAADAARRP	379
Qy	381	SSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSA	440
Db	380	GA-NDGAPDDEDDGASRIFFEPSLYHCLENCGSVLLSVACQGGEGNSTFYVDYRTEDGSA	438
Qy	441	NAGADYEFTEGTVVLKPGETQKEFSVGIIIDDDIFEEDHFFVRLSNVRIEEEQ----PEE	496
Db	439	KAGSDYIEYSEGLTVFKPGETQKELRIGIIDDDIFEEDHFFVRLNLNRVGDAQGMFEPDG	498
Qy	497	GMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRSTS	556

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Db          |          | : | : | : ||||| ||||| : : | : | : | : | : |
499 G-----GRPKGRLVAPLLATVTILDDDHAGIFS FQDRLLHVSECMGTVDVRVVRSS 549

Qy          557 GARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
          ||||| : | : | : ||| : || ||||| : ||| :
Db          550 GARGTVRLPYRTVDGTARGGGVHYEDACGELEFGDDETM 588

```

RESULT 11

B89047

protein C10G8.5 [imported] - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text change 24-May-2001

C;Accession: B89047

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology.

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and

www.sanger.ac.uk/Projects/C_elegans/ for a list of authors

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 285, 1493, 1999

A;Accession: B89047

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-890 <STO>

A;Cross-references: GB:chr_V; PIDN:AAB09172.1; PID:q1572830; GSPDB:GN00023;

CESP:C10G8.5

C; Genetics:

A;Gene: C10G8.5

```
A;Map position: 5
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C;Superfamily: human Na⁺/Ca²⁺-exchanging protein

Query Match 37.1%; Score 1196.5; DB 2; Length 890;

Best Local Similarity 47.6%; Pred. No. 1.9e-83;

Matches 243; Conservative 97; Mismatches 150; Indels 21; Gaps 7;

QY 87 MFLGVSIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAP 146
 |||::|:||||:|||||| || : ::| : :|::|:|||||||
 Db 1 MFLGISIVADRFMSSIEVITSMERTIVVKRPLDPMAVQVRIWNDTVSNLTLMALGSSAP 60

QY 147 EILLSLIEVCGHGFAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRRIKHLRVFFIT 206
 ||||:| | |||||:|||||||:|:| | | | | : | | : |
 Db 61 EILLSIIEVIARGFEAGDLGPNTIVGSAAFNLFMIIAICVWVWIPKGEIRROKHLDVFCVT 120

QY 207 AAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYR 266
| ||: ||: ||: ||: || | || | :: || | | ||: | |:: || :| :| :|
Db 121 ATWSVFAYVWLYLILAFFSPGEIEIWEGALTFIFFPLTVFTAYMADIKLIQNKFLPHRYR 180

Qy 267 TDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQK 326
| | : | | : | : | : | | : | | : | : | :
Db 181 RGSHT-QQMIAEAEEEMKMLE-----NGTQGDPALKAFEEHRQEFIELMREIRKQ 228

QY 327 HPEKDLQLVEMANYYYALSHQQSRAFYRIQATRMMTGAGNILKKHAAEQAKKA-SSMSE 385
:| :| :| | :| |||||:|||| :| |:|:| :: || :::
Db 229 NP HITPTELQKQAEYEMISRGPKSRAFYRVQATRRLIGGGDIVKKRIDKEHNKALDALVO 288

M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: C84917

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-538 <STO>

A;Cross-references: GB:AE002093; NID:g3522931; PIDN:AAC62871.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g47600; T30B22.10

A;Map position: 2

A;Introns: 131/1; 189/3; 229/2; 287/1; 333/1; 397/1; 440/2

Query Match 11.2%; Score 362.5; DB 2; Length 538;
Best Local Similarity 31.3%; Pred. No. 9.3e-20;
Matches 91; Conservative 61; Mismatches 96; Indels 43; Gaps 9;

Qy 64 YPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETST 123
:| :| | : | ::||: | | |:|:| | || |:| : | :| | :
Db 29 FPGENTLSDGL-RGVLYFLGLAYCFIGLSAITARFFKSMENVVKHSRKVVTIDPITKAEV 87

Qy 124 TTI-RVWNETVSNLTLMALGSSAPEILLSLIEV---CGHGFIAGDLGPSTIVGSAAFNMF 179
| :||| |:::|:| | :| | :| :| : | : || ||| |:|||||:|
Db 88 ITYKKVWNFTIADISLLAFGTSFPQISLATIDAIRNMGERY-AGGLPGTTLVGSAAFDLF 146

Qy 180 IIIGICVYVIPDGETRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLF 239
| :|| | || :|| | | : : || :|||||:| | :| | : : | |||:
Db 147 PIHAVCVVVPKAGELKKISDLGVWLVELVWSFWAYIWLYIILEVWSPNVITLVEALLTVL 206

Qy 240 FFPVCVLLAWVADKRLLFYKYMHHKRYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDG 299
: : : | : ||| : | : : : || | :
Db 207 QYGLLLVHAYAQDKR---WPYLS-----LPMSRGDRPE----- 236

Qy 300 NLVPLEGKEVDESR---REMIRILKDLKQKHPEKDLDQLVEMANYYALSH 346
|| :|:| | : : : | | | :|: : : : :
Db 237 EWVP---EEIDTSKDDNDNDVHDVYSDAQAQDAVESGSRNIVDIFSISANN 284

RESULT 14

T31433

Na⁺/Ca²⁺,K⁺-exchanging protein - bottle-nosed dolphin

C;Species: *Tursiops truncatus* (bottle-nosed dolphin)

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T31433

R;Cooper, C.B.; Winkfein, R.J.; Schnetkamp, P.P.M.

submitted to the EMBL Data Library, April 1998

A;Description: Cloning, sequencing, and functional expression of the bottlenose dolphin retinal rod Na/Ca+K exchanger reveals a cytosolic inhibitory domain.

A;Reference number: Z21032

A;Accession: T31433

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1014 <COO>

A;Cross-references: EMBL:AF059031; NID:g3170602; PID:g3170603; PIDN:AAC18119.1
C;Genetics:
A;Gene: NCKXr

Query Match 6.4%; Score 205; DB 2; Length 1014;
Best Local Similarity 23.6%; Pred. No. 2.7e-07;
Matches 105; Conservative 65; Mismatches 161; Indels 114; Gaps 19;

```
Qy      77 VIVYFVALIYMFLGVSIIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN 135
      |:::  ::||:  ::||:  |  |:  ::  |||  :  :::  :|  |:
Db      451 VVLHIFGMLYVFVALAIVCDEYFVPALGVITDK-----LQI-SEDVAG 492

Qy      136 LTLMALGSSAPEILLSLIEVCGHGFIA-GDLGPSTIVGSAAAFNMFIIGICVYVIPDGET 194
      |  ||  |  ||||:  |||  :  ||:  ::|  |||||  ||:  :||  |  :
Db      493 ATFMAAGGSAPLEFTSLIGI----FISHSNVGIGTIVGSAVFNILFVIGTCALF-----S 543

Qy      195 RKIKHLRVFFITAAWSIFAYIWLY-----MILAVFSPGVVQVWEGLLTLFFFPVCVL-LA 248
      |:|  :|  |  :|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      544 REILNL-----TWWPLFRDITFYILDMLLILFFFLDSLIVVWESLLLLLAYALYVFTMK 597

Qy      249 WVADKRLLFYKYMHHK-----YRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGNLV 302
      |  |  |  |  |  :  ::  |  |  :  :  |  |  |  |  |  |  |  |  |  |  |
Db      598 WNKQLELWVKQLSRRPVPKVMALGDLSKGDVAEAS---TGERTDNEVK-----T 645

Qy      303 PLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYYALSHQQK--SRAFYRIQATR 360
      |  ||:  ::|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      646 PGEGENGEQSGGE-----AQPEGEKEEGKGENESEGDIQAERKGENESEGDIQAER 695

Qy      361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      |  |  |  |  |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      696 KGDDEG-----EGEIQAGEDGEMKGDEGD-----LQAER 724

Qy      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGI-----IDD 471
      ||  |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      725 KGDDEGEGEI--QAGEDGEMK-GDDGETGEQDLIADNQDDAKEDEKGIDGEEEGDGGGESE 781

Qy      472 DIFEEDEHFFVRLSNVRIEEEQPEE 496
      |  ||:|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      782 DEEEEEEEGEEEEEQEEEEEQEEE 806
```

RESULT 15

S20969

Na⁺/Ca²⁺,K⁺-exchanging protein - bovine

N;Alternate names: Na⁺/Ca²⁺,K⁺ antiporter; Na/Ca,K-exchanger

C;Species: Bos primigenius taurus (cattle)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C;Accession: S20969

R;Reilaender, H.; Achilles, A.; Friedel, U.; Maul, G.; Lottspeich, F.; Cook, N.J.

EMBO J. 11, 1689-1695, 1992

A;Title: Primary structure and functional expression of the Na/Ca,K-exchanger from bovine rod photoreceptors.

A;Reference number: S20969; MUID:92258377; PMID:1582405

A;Accession: S20969

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1199 <REI>

A;Cross-references: GB:X66481; NID:g505578; PIDN:CAA47108.1; PID:g505579

Query Match 6.1%; Score 198.5; DB 2; Length 1199;
Best Local Similarity 21.7%; Pred. No. 1.1e-06;
Matches 132; Conservative 74; Mismatches 210; Indels 193; Gaps 27;

```
Qy      77 VIVYFVALIYMFLGVSIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN 135
      |:::  ::|:|: ::|: | |: :: ||| :      ::: :| |:
Db      449 VVLHIFGMMYVFVALAIVCDEYFVPALGVITDK-----LQI-SEDVAG 490

Qy      136 LTLMALGSSAPEILLSLIEVCGHGFIA-GDLGPSTIVGSAAFNMFIIGICVYVIPDGET 194
      | || | |||: ||| | ||: ::| ||||| ||: :|| | :
Db      491 ATFMAAGGSAPELFTSLIGV----FISHSNVGIGTIVGSAVFNILFVIGTCALF-----S 541

Qy      195 RKIKHLRVFFITAAWSIFAYIWLY----MILAVFSPGVVQVWEGLLTLFFFFPVCVL-LA 248
      |:| :| | :| | | | |:: | :: || :| | : | :
Db      542 REILNL-----TWWPLFRDITFYIFDLMLLILFFLDSLIAWWESVLLLLLAYAFVFTMK 595

Qy      249 WVADKRLLFYKYMHHK-----YRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDG 299
      | | : ::| : : | : | : | : | : :
Db      596 WNQOLELWVKEQLNKRPAKVMALGDLSPKPGDGTVVVDEQQDNKKLKLSSMLTRG----S 651

Qy      300 NLVPLEGKEVDESRE-MIRILKDLKQKHPEKDLQ--LVEMANYYALSHQQKSRAFYRI 356
      : | : : : |: | | : | || :: |: |
Db      652 SSASLHNSTIRSTIYQLMLHSLDPLGEARPSKDKEEETLIPEAK----- 695

Qy      357 QATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-----DFISKVFFDPCSYQC 407
      | || | | | | | | | | | |
Db      696 -----ATPQAKAESKPEEPAKLPEVTVTPAPAPDVKGDQEEDPGSQGV 739

Qy      408 ---LENCG-----AVLLTVVRKGGDMSKTMVVDYKTEDGS-----ANAGADYEFT 449
      || | | | | | | | | | | | | | |
Db      740 GAEAENTGERTGGEAEAPAEGENGERSGGDAALGGESEGKAENESEGDIPAERRGDDE-D 798

Qy      450 EGTVVLKPGETQKEFSVGII-----DDDIFF-----EDEHFFVRLSNV 487
      || : : || : : | | | : | | | | |
Db      799 EGEIQAEGGEVKGDEDEGEIQAGEGGEVEGDEDEGEIQAGEGGEVEGDEDE-----GEI 852

Qy      488 RIEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGV 547
      : | | | | | | | | | | | | | |
Db      853 QAGEAGEVEG-----DEDEGEIQAGEAGEVEGDEDEGE 885

Qy      548 MEVKVLRTSGARGTVIVPFRTVEGTAKGG-----GEDFEDTYGELEFKNDETVCDRQEA 601
      :: :| | | : || : | || | | :| | |
Db      886 IQ-----AGEGGEV----KGDEGEIQAGEAGEVEGED-----GEVEGGEDEGEIQAGEG 930

Qy      602 DYGRRGQE 610
      | | |
Db      931 GEGETGEQE 939
```

Search completed: June 24, 2004, 16:15:03
Job time : 16.0818 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2004, 16:12:03 ; Search time 34.1986 Seconds
(without alignments)
5118.180 Million cell updates/sec

Title: US-10-054-680-4
Perfect score: 3228
Sequence: 1 MAWLRLQPLTSAFLHFGGLVT.....ADYGRRGGQEDSRDGKASIG 620

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	3228	100.0	620	13	US-10-054-680-4	Sequence 4, Appli
2	3093	95.8	595	14	US-10-256-537-2	Sequence 2, Appli
3	3093	95.8	921	9	US-09-804-474A-2	Sequence 2, Appli
4	3093	95.8	921	13	US-10-054-680-2	Sequence 2, Appli
5	3093	95.8	925	14	US-10-114-153-4	Sequence 4, Appli
6	3093	95.8	927	14	US-10-275-116-2	Sequence 2, Appli
7	3093	95.8	928	14	US-10-114-153-2	Sequence 2, Appli
8	3016	93.4	927	9	US-09-804-474A-4	Sequence 4, Appli
9	2940	91.1	895	14	US-10-114-153-6	Sequence 6, Appli
10	2147.5	66.5	970	9	US-09-901-419-2	Sequence 2, Appli
11	2143.5	66.4	609	9	US-09-864-761-33429	Sequence 33429, A
12	1961	60.7	921	14	US-10-281-866-2	Sequence 2, Appli
13	1196.5	37.1	890	15	US-10-369-493-6319	Sequence 6319, Ap
14	633.5	19.6	807	15	US-10-369-493-6148	Sequence 6148, Ap
15	633.5	19.6	807	15	US-10-369-493-6149	Sequence 6149, Ap
16	243	7.5	161	12	US-10-424-599-228842	Sequence 228842,
17	203.5	6.3	106	14	US-10-256-537-5	Sequence 5, Appli
18	203.5	6.3	661	13	US-10-094-214-5	Sequence 5, Appli
19	203.5	6.3	661	14	US-10-281-868-2	Sequence 2, Appli
20	203.5	6.3	661	15	US-10-391-399-17	Sequence 17, Appl
21	202	6.3	6304	14	US-10-147-026-16	Sequence 16, Appl
22	197	6.1	546	12	US-10-276-774-2632	Sequence 2632, Ap
23	194.5	6.0	500	14	US-10-264-104-2	Sequence 2, Appli
24	186.5	5.8	644	15	US-10-353-690-18	Sequence 18, Appl
25	184	5.7	2092	14	US-10-147-026-12	Sequence 12, Appl
26	180.5	5.6	603	9	US-09-961-679-2	Sequence 2, Appli
27	178.5	5.5	591	15	US-10-369-493-6463	Sequence 6463, Ap
28	178.5	5.5	591	15	US-10-369-493-6464	Sequence 6464, Ap
29	175	5.4	1081	16	US-10-408-765A-298	Sequence 298, App
30	171.5	5.3	2780	12	US-10-423-483-2	Sequence 2, Appli
31	171.5	5.3	2780	15	US-10-220-587-2	Sequence 2, Appli
32	170	5.3	611	15	US-10-369-493-5204	Sequence 5204, Ap
33	162.5	5.0	1577	14	US-10-219-834-150	Sequence 150, App
34	161	5.0	759	15	US-10-415-378-15	Sequence 15, Appl
35	161	5.0	2753	12	US-10-262-511-160	Sequence 160, App
36	161	5.0	2753	12	US-10-262-511-166	Sequence 166, App
37	161	5.0	3838	12	US-10-262-511-162	Sequence 162, App
38	158.5	4.9	1615	14	US-10-219-834-149	Sequence 149, App
39	154	4.8	2777	12	US-10-423-483-4	Sequence 4, Appli
40	154	4.8	2777	15	US-10-220-587-4	Sequence 4, Appli
41	146	4.5	35	12	US-10-423-483-24	Sequence 24, Appl
42	146	4.5	35	15	US-10-220-587-24	Sequence 24, Appl
43	136.5	4.2	461	15	US-10-104-047-2842	Sequence 2842, Ap
44	135.5	4.2	1469	12	US-10-262-511-164	Sequence 164, App
45	133.5	4.1	227	14	US-10-264-104-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-10-054-680-4

; Sequence 4, Application US/10054680

; Publication No. US20020132998A1

; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan

; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and
Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 620
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-054-680-4

Query Match 100.0%; Score 3228; DB 13; Length 620;
Best Local Similarity 100.0%; Pred. No. 5.7e-315;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540

```

Qy      541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVCDRQE 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVCDRQE 600

Qy      601 ADYGRRGGQEDSRDGKASIG 620
      |||||||||||||||
Db      601 ADYGRRGGQEDSRDGKASIG 620

```

RESULT 2

US-10-256-537-2

```

; Sequence 2, Application US/10256537
; Publication No. US20030162196A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
; TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER
; FILE REFERENCE: MPI01-231PlRM
; CURRENT APPLICATION NUMBER: US/10/256,537
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/325,737
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-256-537-2

```

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Query Match          95.8%; Score 3093; DB 14; Length 595;
Best Local Similarity 100.0%; Pred. No. 2e-301;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120

Qy      121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180

Qy      181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240

Qy      241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN 300

Qy      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRIFYRIQATR 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRIFYRIQATR 360

```

```

Qy      361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
          |||
Db      361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
          |||
Db      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
          |||
Db      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy      541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
          |||
Db      541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

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RESULT 3

US-09-804-474A-2

; Sequence 2, Application US/09804474A

; Patent No. US20020119518A1

; GENERAL INFORMATION:

; APPLICANT: KODET, Stefan et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000891

; CURRENT APPLICATION NUMBER: US/09/804,474A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 921

; TYPE: PRT

; ORGANISM: Human

US-09-804-474A-2

Query Match 95.8%; Score 3093; DB 9; Length 921;

Best Local Similarity 100.0%; Pred. No. 4.2e-301;

Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
          |||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120
          |||
Db      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120

Qy      121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180
          |||
Db      121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180

Qy      181 IIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
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Db      181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qy      241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEETEGDHPKGIEMDGKMMNSHFLDGN 300
        |||
Db      241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEETEGDHPKGIEMDGKMMNSHFLDGN 300
Qy      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQDLVEMANYYYALSHQQKSRIFYRIQATR 360
        |||
Db      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQDLVEMANYYYALSHQQKSRIFYRIQATR 360
Qy      361 MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
        |||
Db      361 MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Qy      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
        |||
Db      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
Qy      481 FVRLSNVRIIEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
        |||
Db      481 FVRLSNVRIIEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qy      541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET 595
        |||
Db      541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET 595

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RESULT 4

US-10-054-680-2

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; Sequence 2, Application US/10054680
; Publication No. US20020132998A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and
Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 921
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-054-680-2

```

```

Query Match          95.8%; Score 3093; DB 13; Length 921;
Best Local Similarity 100.0%; Pred. No. 4.2e-301;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 MAWLRLQPLTSAFLHFGVLTFLVFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
        |||
Db      1 MAWLRLQPLTSAFLHFGVLTFLVFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

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Qy	61	PIWYPENPSLGDK IARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDK IARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETR KIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETR KIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRL LFYKYMHKKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRL LFYKYMHKKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRR EMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRR EMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 5

US-10-114-153-4

; Sequence 4, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Shenoy, Suresh

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter

; APPLICANT: Smithson, Glennnda

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Tchernev, Velizar

; APPLICANT: Gangolli, Esha

```

; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 4
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-4

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Query Match          95.8%;  Score 3093;  DB 14;  Length 925;
Best Local Similarity 100.0%;  Pred. No. 4.2e-301;
Matches 595;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy          1 MAWLRLQPLTSAFLHFGVLTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAWLRLQPLTSAFLHFGVLTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy          61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120

```


Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRIFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRIFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRITSGARGTVIVPFRITVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLRITSGARGTVIVPFRITVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 6

US-10-275-116-2

; Sequence 2, Application US/10275116

; Publication No. US20030096312A1

; GENERAL INFORMATION:

; APPLICANT: Merck Patent GmbH

; TITLE OF INVENTION: No. US20030096312A1e1 natrium-calium exchanger protein

; FILE REFERENCE: HNCX3CWWS

; CURRENT APPLICATION NUMBER: US/10/275,116

; CURRENT FILING DATE: 2002-11-01

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 927

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-275-116-2

Query Match 95.8%; Score 3093; DB 14; Length 927;

Best Local Similarity 100.0%; Pred. No. 4.2e-301;

Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRIFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRIFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLRRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 7

US-10-114-153-2

; Sequence 2, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shenoy, Suresh

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter

; APPLICANT: Smithson, Glennnda

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Gangolli, Esha
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Taupier, Raymond J. Jr.
 ; APPLICANT: Heyes, Melvyn
 ; APPLICANT: Ju, Jingfang
 ; APPLICANT: Peyman, John
 ; APPLICANT: Catterton, Elina
 ; APPLICANT: MacDougall, John
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Stone, David
 ; APPLICANT: Mazur, Ann
 ; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
 NUCLEIC ACIDS
 ; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
 ; FILE REFERENCE: 21402-322A
 ; CURRENT APPLICATION NUMBER: US/10/114,153
 ; CURRENT FILING DATE: 2002-08-06
 ; PRIOR APPLICATION NUMBER: 60/281086
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281906
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/282020
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/282930
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/283512
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/283444
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/283657
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283710
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283678
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/284234
 ; PRIOR FILING DATE: 2001-04-17
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 251
 ; SEQ ID NO 2
 ; LENGTH: 928
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-114-153-2

Query Match 95.8%; Score 3093; DB 14; Length 928;
 Best Local Similarity 100.0%; Pred. No. 4.2e-301;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

```

      |||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
Qy      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120
      |||
Db      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120
Qy      121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFI 180
      |||
Db      121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFI 180
Qy      181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF 240
      |||
Db      181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF 240
Qy      241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN 300
      |||
Db      241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN 300
Qy      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQKSRIFYRIQATR 360
      |||
Db      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQKSRIFYRIQATR 360
Qy      361 MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      |||
Db      361 MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Qy      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
      |||
Db      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
Qy      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTIILDDDHAGIFTFECDTIH 540
      |||
Db      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTIILDDDHAGIFTFECDTIH 540
Qy      541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDIV 595
      |||
Db      541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDIV 595

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RESULT 8

US-09-804-474A-4

; Sequence 4, Application US/09804474A

; Patent No. US20020119518A1

; GENERAL INFORMATION:

; APPLICANT: KODET, Stefan et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000891

; CURRENT APPLICATION NUMBER: US/09/804,474A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 927

; TYPE: PRT
; ORGANISM: Rat
US-09-804-474A-4

Query Match 93.4%; Score 3016; DB 9; Length 927;
Best Local Similarity 97.1%; Pred. No. 2.3e-293;
Matches 578; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

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Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
        ||||||||||||||||||||||||||||||||||||||||| |||| ||||||||||||||||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGDLRDVPSAGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
        ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFI 180
        ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFI 180

Qy    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF 240
        |||||||||||||||||||||||||:|||||:||||||||||||||||||||||||||
Db    181 IIGICVYVIPDGETRRIKHLRVFFVTAAWSVFAYIWLYMILAVFSPGVQVWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
        |||||||||||||||||||||||||:|||||:||||||||||||||||||||||||||
Db    241 FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIIETEGEHPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRIFYRIQATR 360
        |:||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    301 LIPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRIFYRIQATR 360

Qy    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
        |||||||||||||||||||||:|||||:||||||||||||||||||||||||||
Db    361 MMTGAGNILKKHAAEQAKKTASMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
        ||||:||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    421 KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy    481 FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
        |||||||:|||| |||| ||| ||||||||||||||||||||||||||||||||
Db    481 FVRLSNVRVEEQLEEGMTPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy    541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET 595
        ||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET 595
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RESULT 9

US-10-114-153-6

; Sequence 6, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 6
; LENGTH: 895
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-114-153-6

Query Match 91.1%; Score 2940; DB 14; Length 895;
Best Local Similarity 99.8%; Pred. No. 9.7e-286;
Matches 565; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      30 AEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL 89
      :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 SEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL 61

Qy     90 GVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEIL 149
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 GVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEIL 121

Qy    150 LSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKHHLRVFFITA AW 209
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 LSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKHHLRVFFITA AW 181

Qy    210 SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDK 269
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDK 241

Qy    270 HRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRREMIRILKDLKQKHPE 329
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 HRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRREMIRILKDLKQKHPE 301

Qy    330 KDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD 389
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 KDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD 361

Qy    390 EPEDFISKVFFDPCSYQCLNCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFT 449
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 EPEDFISKVFFDPCSYQCLNCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFT 421

Qy    450 EGTVVLKPGETQKEFSVGIIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP 509
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 EGTVVLKPGETQKEFSVGIIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP 481

Qy    510 RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTV 569
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTV 541

Qy    570 EGTAKGGGEDFEDTYGELEFKNDETV 595
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Db    542 EGTAKGGGEDFEDTYGELEFKNDETV 567
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RESULT 10

US-09-901-419-2

; Sequence 2, Application US/09901419

; Patent No. US20020069421A1

; GENERAL INFORMATION:

; APPLICANT: The Curators of the University of Missouri

; TITLE OF INVENTION: LARGE SCALE EXPRESSION AND PURIFICATION OF RECOMBINANT

; TITLE OF INVENTION: PROTEINS

; FILE REFERENCE: UMO1531.1

; CURRENT APPLICATION NUMBER: US/09/901,419

; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/218,125
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 970
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-901-419-2

Query Match 66.5%; Score 2147.5; DB 9; Length 970;
Best Local Similarity 69.4%; Pred. No. 5.7e-206;
Matches 422; Conservative 74; Mismatches 91; Indels 21; Gaps 8;

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Qy      1 MAWLRLQPLTSAFLHFGVLTFVLF--LNGLRAEAGSGDVPSTGQNNESCSGSSDCKEGV 58
      | | | | | : | | : | | | | | | | | | | | | | | | | | | | | |
Db      1 MLQFSLSPTLSMGFHVIA MVALLFSHVDHISAETEMEGEGNETGE----CTGSYYCKKGV 56

Qy      59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN 118
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      57 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN 116

Qy     119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIA GDLGPSTIVGSAAFNM 178
      | | | : | | : | | | | | | | | | | | | | | | | | | | | | |
Db     117 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 176

Qy     179 FIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL 238
      | | | | : | | | : | | | | | | | | | | | | | | | | | | | |
Db     177 FIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEWEGLLTF 236

Qy     239 FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH 295
      | | | | : | | | : | | | | | | | | | | | | | | | | | | | |
Db     237 FFFPICVFAWVADRRLLFYKYVYKRYRAGKQ RGMIIIEHEGDRPSSKTEIEMDGKVNSH 296

Qy     296 ---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 348
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     297 VDSFLDGALV-LEVDERDQDDEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355

Qy     349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS YQC 407
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     356 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGT YQC 415

Qy     408 LENC GAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     416 LENC GTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

Qy     468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     476 IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVS---TLACLGSPSTATVTIFDDD 532

Qy     528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy     588 EFKNDETV 595
      | | : | | | |
```


RESULT 11

US-09-864-761-33429

; Sequence 33429, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 33429

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; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007281.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
; OTHER INFORMATION: EST_HUMAN HIT: AW452398.1, EVALUE 1.00e-49
; OTHER INFORMATION: SWISSPROT HIT: P32418, EVALUE 0.00e+00
US-09-864-761-33429
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Query Match          66.4%; Score 2143.5; DB 9; Length 609;
Best Local Similarity 69.3%; Pred. No. 6.6e-206;
Matches 420; Conservative 76; Mismatches 89; Indels 21; Gaps 8;
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Qy      1 MAWLRLQPLTSAFLHFGVLTFVLF--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
      | | | | | : : | : : | | : | | : | | : | |
Db     11 MRRLSLSPTFSMGFHLTVSLLFSHVDHVIAETEMEGETGE----CTGSYYCKKGV 66

Qy     59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN 118
      | | | | | : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     67 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN 126

Qy    119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNM 178
      | | | : | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    127 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 186

Qy    179 FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL 238
      | | | : | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    187 FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF 246

Qy    239 FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH 295
      | | | : | | : | | | | | | | | : : | | | | | | | | | | | | | | | | | |
Db    247 FFFPICVVFVAVADRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPSSKTEIEMDGKVNSH 306

Qy    296 ---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 348
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    307 VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLSQQQ 365

Qy    349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    366 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVTENDPVSKIFFEQGTYYQC 425

Qy    408 LENC GAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    426 LENC GTVALTIIRRGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGDTQKEIRVG 485

Qy    468 IIDD DIFEED EHHFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    486 IIDD DIFEED ENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD 542

Qy    528 HAGIFTFECDTIHVSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
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Db      543 HAGFTFEEPVTHVSESIGIMEVKVLR TSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 602

Qy      588 EFKNDE 593
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Db      603 EFQNDE 608

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RESULT 12

US-10-281-866-2

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; Sequence 2, Application US/10281866
; Publication No. US20030091570A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and compositions for the
; TITLE OF INVENTION: treatment and diagnosis of pain disorders using 46556
; FILE REFERENCE: MPI01-272P1RM
; CURRENT APPLICATION NUMBER: US/10/281,866
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/335,078
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-281-866-2

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Query Match          60.7%; Score 1961; DB 14; Length 921;
Best Local Similarity 65.7%; Pred. No. 3e-187;
Matches 371; Conservative 87; Mismatches 83; Indels 24; Gaps 6;

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Qy      40 STGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFM 99
          ||| | | | | | | | | | | | | | | | | | | | | |
Db      39 STG-----GCQGSYRCQPGVLLPWPEDDPSLGDKAARAVVYFVAMVYMFLGVSIIADRFM 94

Qy      100 ASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHG 159
          |:| | | | | | | | | | | | | | | | | | | | | |
Db      95 AAIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHN 154

Qy      160 FIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYM 219
          | | | | | | | | | | | | | | | | | | | | | |
Db      155 FQAGELGPGTIVGSAAFNMFVVIACVIYVIPAGESRRIKHLRVFFVTASWSIFAYVWLYL 214

Qy      220 ILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEG 279
          ||||| | | | | | | | | | | | | | | | | | |
Db      215 ILAVFSPGVVQVWEALLTLVFFPVCVFAWMADKRLLFYKYVYKRYRTDPRSGIIIGAEG 274

Qy      280 DHPKGIEMDGKMMNSHFLDGNL-----VPLEGKEVDESRRMIRILKDLKQKHPEKDLDQ 334
          | | | | | | | | | | | | | | | | | | | | | |
Db      275 DPPKSIELDGTFFVGAE-APGELGGLPGPAEARELDASRREVIQILKDLKQKHDPKDLEQ 333

Qy      335 LVE MANY YALSHQKSR AFYRIQATRM MTGAGN I LK KHAAEQAKKASSMSEVHTDEPEDF 394
          || :| | | | | | | | | | | | | | | | | | | | |
Db      334 LVGIANY YALLHQKSR AFYRIQATRLMTGAGN VLR RHAADASRRAPAEGAGEDD- DDG 392

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Qy	395	ISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVV	454
		:: : : :: : : : :: : :: :	
Db	393	ASRIFFEPSLYHCLENCGSVLLSVTCQGGEKNSTFYVDYRTEDGSAKAGSDYSEGLV	452
Qy	455	LKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQ----PEEGMPPAIFNSLPLPR	510
		: ::: :: :	
Db	453	FKPGETQKELRIGIIDDDIFEEDHFFVRLNLNRVGDAQGMFEPDGG-----GRPK	503
Qy	511	AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVE	570
		: : : : : :: : : : : :: :	
Db	504	GRLVAPLLATVTILDDDHAGIFSQDRLLHVSECMGTVDVRVVRSSGARGTVRLPYRTVD	563
Qy	571	GTAKGGGEDFEDTYGELEFKNDETV	595
		: : : :	
Db	564	GTARGGGVHYEDACGELEFGDDETM	588

US-10-369-493-6319

2. TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

US-10-369-493-6319

Qy	87	MFLGVSIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAP	146
		: : : : : : : : : :	
Db	1	MFLGISIVADRFMSSIEVITSMERTIVVKRPGLDPMVQVRIWNDTVSNLTLMALGSSAP	60
Qy	147	EILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKIKHLRVFFIT	206
		: : : : : :	
Db	61	EILLSIIEVIARGFEAGDLGPNTIVGSAAFNLFMIIAICVVVIPKGEIRROKHLDFVCVT	120
Qy	207	AAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYR	266
		: : : : : : : : : : : : : :	
Db	121	ATWSVFAYVWLYLILAFFSPGEIEIWEGALTFIFFPLTVFTAYMADIKLIQNKFLPHRYR	180

Qy	267	TDKHRGIIETEGTDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRREMIRILKDLKQK	326
Db	181	RGSH-GQMIATEAEEMKMLE-----NGTQGDPAKAFEEHRQEFIELMREIRKQ	228
Qy	327	HPEKDLDLQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKA-SSMSE	385
Db	229	NPHITPTELQKQAEYEMISRGPKSRAFYRVQATRRLIGGGDIVKKRIDKEHNKALDALVQ	288
Qy	386	VHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGAD	445
Db	289	AQEKQSRDNTCKIFLDPAHYTVLESVGSFDDVVVGRDGGPDGLTVMVDYFTEDGSANAGSD	348
Qy	446	YEFTEGTVVLKPGETQKEFSVGIIIDDDIFEDEHFFVRLSNVRIEEEQPEEG--MPPAIF	503
Db	349	YIPVKGTLTTFYPEDKHQKVITIEVDDDDVFEDEHFYLRCLNLRV---RTKDGIIDPTRI	405
Qy	504	NSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVI	563
Db	406	GGLPV--AQLEMPNTATIMILDDDHAGVFGFEHDFQVVENCGHLSLQMKRHSGARGKVI	463
Qy	564	VPFRTVEGTAKGGGEDFEDTYGELEFKNDET	594
Db	464	IPFRTVEGTA-SADKHFEEMKEGEIVFEDNOT	493

US-10-369-493-6148

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEO ID NO 6148

; LENGTH: 807

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-369-493-6148

Best Local Similarity 29.1%; Pred. No. 7.9e-54;

Matches 174; Conservative 96; Mismatches 174; Indels 153; Gaps 18;

QY 47 SCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVIT 106
| | : | | :: | : | : | | :: | | | | |

Db 2 SSSANLTCKNGILI-----PALETTTPRNAILYLAGLFYCFGLGIAIAADIFMCSIEQIT 54

Qy 107 SQEREVTIKKPNGETSTTT-----IRVWNETVSNLTLMALGSSAPEILLSLIEV 155
| : : | : | : : : | | : | | | | | | | | | | | | : | :

Db 55 SATKKVKKQKKAGQLVAKEEDEEIDEQYDYVRIWNPTVANLTLMALGSSAPEILLSSIIEI 114

Qy 156 CGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYI 215
| : | | | | | | | | | | | | : | | : : : : | | : | : | | |

Db 115 VGNGFKAGDLGPGTIVGSAAFNLFCSAICVFAV-GTQTKRIELRYRVFVVTAFFGTFAI 173

Qy 216 WLYMILAVFSPGVVQVWEGLLTLFFFFPVCVLLAWVADKRLLFYKYMHHKYRTD----- 268
| : : : | | : | | | | : | | | : : : : | : : | | : |

Db 174 WVFLVLIVITPNVVDVWEAILTLLFFIILVVVSYAVDAQI-----WKKKKSSDLQEELEM 228

Qy 269 -KHRGIIIETEGDHPKGIEMDGMMNSHFL----DGNLVPLEGKEVDESRR----- 314
: | | : | | : : | | : : : : | | |

Db 229 AQHDGKV----DDQPEKLSDEIKKWASNLSLNKEENDVIVDATPSVDTVRRWTRTSISHTY 284

Qy 315 -----EMIRILKDLKQKHPEKDLQVLVEMANYYALSHQQ 348
| | : : | : : : : | | :

Db 285 PSLSDDEDQAKILAYRVSRTMSHDRLYRIRAIRQLSSSWRKSEEEVLKMNQESTDSAS 344

Qy 349 KSRAF-----YRIQAT-----RMMTGAGNILLKHAAEQAK-----KASSM 383
: : | | : | | : | | : | | : : :

Db 345 RRKTFVEFSARVYRVDATDETVSLKIERKGNMESKFTVSYATVNGLAKKDLNLFKSETL 404

Qy 384 ----SEVH-----TDEPEDFISKVFFDPC--SYQCLENCG 412
| : | | | | | | | | : : | | |

Db 405 QFNPGELHKTISIQLINAAANWRPNDFYVHLKIQDVDED--SKICLGACNVAHVVKENAG 462

Qy 413 AVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADY-EFTEGTVVLKPGETQKEFSVGIIDD 471
| | : | | : | | : | | : | : : | : | : : | |

Db 463 FSRSFVTRRGGLKKPLQVHYETEDVTAKQGDDYTAVKDGILGFEGQEYKEYIDIDVIDD 522

Qy 472 DIFEEDHFFVRLSNVRIEEEQPEEGMPAIFNSLPLPRAVLASPCVATVTILDDDH 528
: | : | | : | : : : | | : : | | : | | :

Db 523 KMDEKDEAFIIEI--LKVDE-----PGVSIGTRRKATITIIISDDN 560

RESULT 15

US-10-369-493-6149

; Sequence 6149, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

```
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6149
; LENGTH: 807
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6149
```

```
Query Match          19.6%; Score 633.5; DB 15; Length 807;
Best Local Similarity 29.1%; Pred. No. 7.9e-54;
Matches 174; Conservative 96; Mismatches 174; Indels 153; Gaps 18;
```

```
Qy      47 SCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVIT 106
      | | : | | |::      | : |      | : | | | |:: | | | | | | |
Db      2 SSSANLTCKNGILI-----PALETTPRNAILYLAGLFYCFLGIAIAADIFMCSIEQIT 54

Qy     107 SQEREVTIKKPNGETSTTT-----IRVWNETVSNLTLMALGSSAPEILLSLIEV 155
      | : : | : | : |      : | : | | | | | | | | | | | | | : | :
Db      55 SATKKVKKQKKAGQLVAKEEDEEIDEQYDYVRIWNPTVANLTLMALGSSAPEILLSIIEI 114

Qy     156 CGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKHKLHVRFFITAAWSIFAYI 215
      | : | | | | | | | | | | | | | | | | | : : : : | | : | : | | |
Db     115 VGNGFKAGDLGPGTIVGSAAFNLFCSAICVFAV-GTQTKRIELRVFVVTAFFGT FayI 173

Qy     216 WLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTD----- 268
      | : : : | | : | | | | : | | | : | : : : | : :      | | : |
Db     174 WVFLVLIVITPNVVDVWEAILTLFFFIILVVVSYAVDAQI-----WKKKKSSDLQEELEM 228

Qy     269 -KHRGIIIETEGDHPKGIEMDGKMMNSHFL----DGNLVPLEGKEVDESRR----- 314
      : | | :      | | : : : | | :      : : :      | | | |
Db     229 AQHDKGV----DDQPEKLSDEIKKWASNLSLNKEENDVIVDATPSVDTVRRWTRTSISHTY 284

Qy     315 -----EMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 348
      | | : : |      : : : : : | | :
Db     285 PSLSDEDQAKILAYRVSRMTSHDRLYRIRAIRQLSSSWRKSEEEVLKMMENQESTDSAS 344

Qy     349 KSRAF-----YRIQAT-----RMMTGAGNILKKHAAEQAK-----KASSM 383
      : : |      | | : | |      : | | : |      | : : :
Db     345 RRKTFVEFSARVYRVDATDET VSLKIERKGNMESKFTVSYATVNGLAKKDLNFLFKSETL 404

Qy     384 ----SEVH-----TDEPEDFISKVFFDPC--SYQCLENCG 412
      | : |      | | | | | : | : : | | |
Db     405 QFNPGELHKTISIQLINAANWRPNDFYVHLKIQDVDED--SKICLGACNVAHVVKENAG 462

Qy     413 AVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADY-EFTEGTVVLKPGETQKEFSVGIIDD 471
      | | : | | : | | : | | : | | : | : : | : | : : | |
Db     463 FSRSFVTRRGKLLKPLQVHYETEDVTAKQGDDYTAVKDGILGFEGQEYKYIDIDVIDD 522

Qy     472 DIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDH 528
      : | : | | : | : : : |      | : : | | : | | : | |
Db     523 KMDEKDEAFIIEI--LKVDE-----PGVSIGTRRKATITIIISDDN 560
```

```
Search completed: June 24, 2004, 16:17:31
Job time : 36.1986 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2004, 16:06:37 ; Search time 32.9916 Seconds
(without alignments)
5929.434 Million cell updates/sec

Title: US-10-054-680-4
Perfect score: 3228
Sequence: 1 MAWLRLQPLTSAFLHFGLVT.....ADYGRRGGQEDSRDGKASIG 620

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length DB	ID			Description

1	3093	95.8	924	4	Q96QG1	Q96qg1 homo sapien
2	3093	95.8	925	4	Q96QG2	Q96qg2 homo sapien
3	3012	93.3	595	11	Q9EPU8	Q9epu8 mus musculu
4	3012	93.3	921	11	Q7TS90	Q7ts90 mus musculu
5	3012	93.3	928	11	Q8VHJ8	Q8vhj8 mus musculu
6	2716	84.1	607	11	Q8BXN1	Q8bxn1 mus musculu
7	2315	71.7	771	4	Q86Y47	Q86y47 homo sapien
8	2157	66.8	934	6	O97801	O97801 macaca mula
9	2156.5	66.8	941	6	Q28662	Q28662 oryctolagus
10	2154.5	66.7	602	6	Q9TV05	Q9tv05 macaca mula
11	2136.5	66.2	941	6	Q9TS14	Q9ts14 oryctolagus
12	2133	66.1	934	11	Q9R238	Q9r238 rattus norv
13	2131	66.0	934	11	Q9WU30	Q9wu30 rattus norv
14	2129	66.0	957	11	Q9R239	Q9r239 rattus norv
15	2128.5	65.9	600	11	Q91ZJ7	Q91zj7 mus musculu
16	2126.5	65.9	600	11	Q9ET74	Q9et74 mus musculu
17	2124	65.8	962	11	Q924Y2	Q924y2 rattus norv
18	2124	65.8	969	11	Q9WU29	Q9wu29 rattus norv
19	2102	65.1	583	13	Q91850	Q91850 xenopus lae
20	2099.5	65.0	940	11	O35157	O35157 mus musculu
21	2030	62.9	968	13	Q9PT19	Q9pt19 oncorhynchu
22	1962.5	60.8	921	11	Q8K596	Q8k596 mus musculu
23	1961	60.7	963	13	Q7T3T7	Q7t3t7 oreochromis
24	1846.5	57.2	706	11	Q8BxB3	Q8bxb3 mus musculu
25	1679	52.0	323	4	Q86TQ9	Q86tq9 homo sapien
26	1501	46.5	892	5	O02196	O02196 loligo opal
27	1339.5	41.5	950	5	Q9VDG5	Q9vdg5 drosophila
28	1339.5	41.5	950	5	Q24413	Q24413 drosophila
29	1328	41.1	950	5	O18367	O18367 drosophila
30	1288	39.9	925	5	O45630	O45630 caenorhabdi
31	1288	39.9	925	5	Q8MYP6	Q8myp6 caenorhabdi
32	1285.5	39.8	950	5	Q8I7I8	Q8i7i8 caenorhabdi
33	1285.5	39.8	975	5	Q8MYP5	Q8myp5 caenorhabdi
34	1278	39.6	254	13	Q9YH83	Q9yh83 gallus gall
35	1278	39.6	793	4	Q9H021	Q9h021 homo sapien
36	1160	35.9	880	5	Q21609	Q21609 caenorhabdi
37	1105.5	34.2	263	13	Q9YGE0	Q9yge0 oncorhynchu
38	1046.5	32.4	263	13	Q9YH84	Q9yh84 gallus gall
39	1038	32.2	264	13	Q9YGE1	Q9yge1 oncorhynchu
40	970.5	30.1	267	13	Q9YGE2	Q9yge2 oncorhynchu
41	660	20.4	199	11	Q8R505	Q8r505 mus musculu
42	655	20.3	560	13	Q91849	Q91849 xenopus lae
43	633.5	19.6	807	5	Q21895	Q21895 caenorhabdi
44	523.5	16.2	171	11	Q8R504	Q8r504 mus musculu
45	519	16.1	215	11	Q9Z0T8	Q9z0t8 rattus norv

ALIGNMENTS

RESULT 1

Q96QG1

ID	Q96QG1	PRELIMINARY;	PRT;	924 AA.
AC	Q96QG1;			
DT	01-DEC-2001	(TrEMBLrel. 19, Created)		
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)		
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)		

DE Sodium/calcium exchanger SCL8A3.
GN SCL8A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bortoluzzi S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Gabellini N.;
RT "Characterization of the human SCL8A3 gene for solute carrier family
RT 8, member 3 (sodium/calcium exchanger).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ304853; CAC40985.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR004837; NaCa_Exmemb.
DR InterPro; IPR004836; Na_Ca_Ex.
DR Pfam; PF03160; Calx-beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMS; TIGR00845; caca; 1.
SQ SEQUENCE 924 AA; 102694 MW; A0A556B753998A07 CRC64;

Query Match 95.8%; Score 3093; DB 4; Length 924;
Best Local Similarity 100.0%; Pred. No. 9.2e-245;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360

Qy 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
 |||
 Db 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
 |||
 Db 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 |||
 Db 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
 |||
 Db 541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

RESULT 2

Q96QG2

ID Q96QG2 PRELIMINARY; PRT; 925 AA.
 AC Q96QG2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Sodium/calcium exchanger SCL8A3.
 GN SCL8A3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bortoluzzi S.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gabellini N.;
 RT "Characterization of the human SCL8A3 gene for solute carrier family
 RT 8, member 3 (sodium/calcium exchanger).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ304852; CAC40984.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 SQ SEQUENCE 925 AA; 102803 MW; 0CCF8DA0881C4FDA CRC64;

Query Match 95.8%; Score 3093; DB 4; Length 925;
 Best Local Similarity 100.0%; Pred. No. 9.2e-245;

Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
      |||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120
      |||
Db     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
      |||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180

Qy    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF 240
      |||
Db    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHHKRYTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
      |||
Db    241 FPVCVLLAWVADKRLLFYKYMHHKRYTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRFYRIQATR 360
      |||
Db    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRFYRIQATR 360

Qy    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      |||
Db    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
      |||
Db    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy    481 FVRLSNVRIEEEQPEEGMPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
      |||
Db    481 FVRLSNVRIEEEQPEEGMPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy    541 VSESIGVMEVKVLRITSGARGTVIVPFRITVEGTAKGGGEDFEDTYGELEFKNDET 595
      |||
Db    541 VSESIGVMEVKVLRITSGARGTVIVPFRITVEGTAKGGGEDFEDTYGELEFKNDET 595

```

RESULT 3

Q9EPU8

ID Q9EPU8 PRELIMINARY; PRT; 595 AA.

AC Q9EPU8;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Sodium-calcium exchanger 3 (Fragment).

GN SLC8A3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.
 RA Sokolow S., Herchuelz A., Schurmans S.;
 RT "Mus musculus mRNA for sodium-calcium exchanger 3 (NCX3), partial
 RT sequence."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF321404; AAG42826.2; -.
 DR MGD; MGI:107976; Slc8a3.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 1.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 FT NON_TER 595 595
 SQ SEQUENCE 595 AA; 66200 MW; 8EF81CBC6EDB7854 CRC64;

Query Match 93.3%; Score 3012; DB 11; Length 595;
 Best Local Similarity 97.5%; Pred. No. 2.1e-238;
 Matches 580; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNCLRAEAGDSDVPVPSAGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFVITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFVITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	FTPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKTSSMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
		:	
Db	421	KGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540

Db 481 FVRLSNVRVEEEQLAEGMLPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 Qy 541 VSESIGMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
 Db 541 VSESIGMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDAYGELEFKNDETV 595

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Q7TS90
ID   Q7TS90          PRELIMINARY;          PRT;          921 AA.
AC   Q7TS90;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Slc8a3 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC052435; AAH52435.1; -.
SQ   SEQUENCE      921 AA;  102376 MW;  50BCBD4DBE8A248A CRC64;

```

Qy 1 MAWLRLQPLTSAFLHFGVLTFVLFLNGLRAEAGGSGDVPSTGONNESC SGSSDCKEGVIL 60

Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNCLRAEAGDSGDVPSAGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRVEEQLAEGMLPAIINSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 5

Q8VHJ8

ID Q8VHJ8 PRELIMINARY; PRT; 928 AA.
AC Q8VHJ8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sodium/calcium exchanger.
GN SLC8A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skeletal muscle;
RA Kraev A.;

Qy 541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDAYGELEFKNDETV 595

RESULT 6

Q8BXN1

ID Q8BXN1 PRELIMINARY; PRT; 607 AA.
 AC Q8BXN1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Solute carrier family 8 (Fragment).
 GN SLC8A3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Retina;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK044636; BAC32013.1; -.
 DR MGD; MGI:107976; Slc8a3.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 1.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 FT NON_TER 607 607
 SQ SEQUENCE 607 AA; 68349 MW; 2762880AF5DEE19D CRC64;

Query Match 84.1%; Score 2716; DB 11; Length 607;
 Best Local Similarity 94.1%; Pred. No. 4.5e-214;
 Matches 524; Conservative 6; Mismatches 27; Indels 0; Gaps 0;

Qy 39 PSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRF 98
 | |: :
 Db 3 PVQGR TMSPVRGHQ TARRVSFCQLWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRF 62
 Qy 99 MASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGH 158
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Db 63 MASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGH 122
 Qy 159 GFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETR KIKHLRVFFITAAWSIFAYIWLY 218
 |||||||||||||||||||||||||||||||||||||||||||||:|||||||

Db 123 GFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRRIKHLRVFFVTAAWSIFAYIWLY 182

Qy 219 MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIETE 278
 |||

Db 183 MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIETE 242

Qy 279 GDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEM 338
 |||

Db 243 GDHPKGIEMDGKMMNSHFLDGNFTPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEM 302

Qy 339 ANYYALSHQQKSRAFYRIQATRMMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKV 398
 |||

Db 303 ANYYALSHQQKSRAFYRIQATRMMTGAGNIIKKHAAEQAKKTSSMSEVHTDEPEDFASKV 362

Qy 399 FFDPCSQCLENCGAVLLTVVRKGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPG 458
 |||

Db 363 FFDPCSQCLENCGAVLLTVVRKGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPG 422

Qy 459 ETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCV 518
 |||

Db 423 ETQKEFSVGIIDDDIFEEDHFFVRLSNVRVEEEQLAEGMLPAILNSLPLPRAVLASPCV 482

Qy 519 ATVTILDDDHAGIFTFECDTIHVSESIGMEVKVLRITSGARGTVIVPFRTVEGTAKGGGE 578
 |||

Db 483 ATVTILDDDHAGIFTFECDTIHVSESIGMEVKVLRITSGARGTVIVPFRTVEGTAKGGGE 542

Qy 579 DFEDTYGELEFKNDETV 595
 |||

Db 543 DFEDAYGELEFKNDETV 559

RESULT 7

Q86Y47

ID Q86Y47 PRELIMINARY; PRT; 771 AA.

AC Q86Y47;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Na⁺/Ca²⁺ exchanger isoform 4 (Fragment).

GN NACAIS4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Lindgren R.M., Bongcam-Rudloff E., Nister M., Heller S.;

RT "Homo sapiens partial mRNA for Na⁺/Ca²⁺ exchanger isoform 4.";

RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ508602; CAD48420.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.

DR GO; GO:0006816; P:calcium ion transport; IEA.

DR InterPro; IPR003644; Calx_beta.

DR InterPro; IPR004837; NaCa_Exmemb.

DR InterPro; IPR004836; Na_Ca_Ex.

DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 1.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 FT NON TER 1 1
 SQ SEQUENCE 771 AA; 86146 MW; A204AAA48A52ED8B CRC64;

Query Match 71.7%; Score 2315; DB 4; Length 771;
 Best Local Similarity 99.6%; Pred. No. 5.5e-181;
 Matches 443; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	151	SLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRRIKHLRVFFITAAWS	210
Db	1	SLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRRIKHLRVFFITAAWS	60
Qy	211	IFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKH	270
Db	61	IFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKH	120
Qy	271	RGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPEK	330
Db	121	RGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPEK	180
Qy	331	DLQDLVEMANYYALSHQQKSRIFYRIQATRMGTAGNIIKKHAAEQAKKASSMSEVHTDE	390
Db	181	DLQDLVEMANYYALSHQQKSRIFYRIQATRMGTAGNIIKKHAAEQAKKASSMSEVHTDE	240
Qy	391	PEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTE	450
Db	241	PEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTE	300
Qy	451	GTVVLKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR	510
Db	301	GTVVLKPRETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR	360
Qy	511	AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVE	570
Db	361	AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVE	420
Qy	571	GTAKGGGEDFEDTYGELEFKNDET	595
Db	421	GTAKGGGEDFEDTYGELEFKNDET	445

RESULT 8

O97801

ID O97801 PRELIMINARY; PRT; 934 AA.
 AC O97801;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Sodium-calcium exchanger isoform NCX1.3.
 GN NCX1.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=99175198; PubMed=10075718;
 RA Li X.F., Lytton J.;
 RT "A circularized sodium-calcium exchanger exon 2 transcript.";
 RL J. Biol. Chem. 274:8153-8160(1999).
 DR EMBL; AF107593; AAD04173.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAJ_2; 1.
 SQ SEQUENCE 934 AA; 104331 MW; 2A228DA30254BBC2 CRC64;

Query Match 66.8%; Score 2157; DB 6; Length 934;
 Best Local Similarity 68.7%; Pred. No. 6.9e-168;
 Matches 426; Conservative 76; Mismatches 90; Indels 28; Gaps 9;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLF--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV	58
		: : : : :	
Db	1	MRRLSLSPTFSMGFHLVIVALLFSHVDYVIAETEMEGEGNETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN	118
		: :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIA GD LGPSTIVGSAAFNM	178
		: : :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGD LGPSTIVGSAAFNM	176
Qy	179	FIIIGICVYVIPDGETR K I K H L R V F F I T A A W S I F A Y I W L Y M I L A V F S P G V V Q V W E G L L T L	238
		: : : :	
Db	177	FIIIALCVYVVPDGETR K I K H L R V F F V T A A W S I F A Y T W L Y I I L S V I S P G V V E V W E G L L T F	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYM HK KYRTDKHRGII I E T E G D H P K G --- I E M D G K M M N S H	295
		: : : : :	
Db	237	FFFPICVVF A W A D R R L L F Y K Y V K R Y R A G Q R G M I I E H E G D R P S S K T E I E M D G K V V N S H	296
Qy	296	---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ	348
		: : : :	
Db	297	VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355
Qy	349	KSRAFYRIQATRM MT G A G N I L K K H A A E Q A K K A S S M S E V H T D E P E - D F I S K V F F D P C S Y Q C	407
		: : : : : :	
Db	356	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVTENDPVSKIFFEQGTYQC	415

QY 408 LENC GAVLLTVVRKGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
 ||||| | ||::||::||::||::||::||::||::||::||::||::||::||::||::||
 Db 416 LENC GTVALTIIRRGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

QY 468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
 ||||| ||||::| | ||||:: | |::| | | | | | | | | | | | | | | | | | | | |
 Db 476 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD 532

QY 528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

QY 588 EFKNDETV-----CDRQE 600
 ||::||| | ||::|
 Db 593 EFQND EIVKIITIRIFDREE 612

RESULT 9

Q28662

ID Q28662 PRELIMINARY; PRT; 941 AA.
 AC Q28662;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Renal Na/Ca exchanger NACA-2.
 GN NCX1.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=92321271; PubMed=1621815;
 RA Reilly R.F., Shugrue C.A.;
 RT "cDNA cloning of a renal Na(+)-Ca2+ exchanger.";
 RL Am. J. Physiol. 262:F1105-F1109(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Reilly R.F., Shugrue C.A.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U52665; AAA97928.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAJ_2; 1.
 SQ SEQUENCE 941 AA; 105128 MW; 7E11396DE70A4084 CRC64;

Query Match 66.8%; Score 2156.5; DB 6; Length 941;
Best Local Similarity 68.8%; Pred. No. 7.7e-168;
Matches 421; Conservative 77; Mismatches 87; Indels 27; Gaps 9;

Qy	8	PLTSAPLHFGVLTVFLF-LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPE	66
Db	9	PFSMGFHLAIVALFFFRVDHVSAAETEMELEGNETGE---CTGSYYCKKGVLPIWEPQ	64
Qy	67	NPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTI	126
Db	65	DPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPNGETTKTTV	124
Qy	127	RVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIGICV	186
Db	125	RIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIALCV	184
Qy	187	YVIPDGETRRIKHLRVFFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFFFPVCVL	246
Db	185	YVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGIVEVWEGLLTFFFFPICVV	244
Qy	247	LAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH---FLDGN	300
Db	245	FAWVADRRLLFYKYVYKRYRAGKQRGMIIEHEGDRPSSKTEIEMDGKVVNSHVDNFLDGA	304
Qy	301	LVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRAFYRI	356
Db	305	LV-LDVERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQKSRAFYRI	363
Qy	357	QATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLENCGAVL	415
Db	364	QATRLMTGAGNILKRHAADQARKAVSMHEVNTEMAENDPVSKIFFEQGTQCLENCGTVA	423
Qy	416	LTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFE	475
Db	424	LTIIRRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVGIIDDDIFE	483
Qy	476	EDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDAGIFTFE	535
Db	484	EDENFLVHLSNVKVSSETSEDGILEANHIS---TLACLGSPCTATVTIFDDDAGIFTFE	540
Qy	536	CDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	ESVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGELEFQNDIV	600
Qy	596	-----CDRQE 600	
Db	601	KIITIRIFDREE 612	

RESULT 10

Q9TV05

ID Q9TV05 PRELIMINARY; PRT; 602 AA.

AC 09TV05;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13. Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Sodium-calcium exchanger circular exon 2 transcript.
 GN NCX1.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=99175198; PubMed=10075718;
 RA Li X.F., Lytton J.;
 RT "A circularized sodium-calcium exchanger exon 2 transcript."
 RL J. Biol. Chem. 274:8153-8160(1999).
 DR EMBL; AF109888; AAD04174.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 1.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAJ_2; 1.
 SQ SEQUENCE 602 AA; 67369 MW; F46C6D8D1D32040E CRC64;

Query Match 66.7%; Score 2154.5; DB 6; Length 602;
 Best Local Similarity 69.6%; Pred. No. 5.7e-168;
 Matches 423; Conservative 75; Mismatches 89; Indels 21; Gaps 8;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLF--LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV	58
		: : : : : : : : : : : : :	
Db	1	MRRLSLSPTFSMGFHLIVIVALLFSHVDYVIAETEMEGEGNETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN	118
		: : : : : : : : : : : : : : :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAAFNM	178
		: : : : : : : : : : : : : : :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAAFNM	176
Qy	179	FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL	238
		: : : : : : : : : : : : : : :	
Db	177	FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH	295
		: : : : : : : : : : : : : : :	
Db	237	FFFPICVFAWVADRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPSSKTEIEMDGKVVNSH	296
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQ	348
		: : : : :	
Db	297	VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355

Qy	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMEVHTDEPE-DFISKVFFDPCSYQC	407
Db	356	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVTENDPVSKIFFEQGTYQC	415
Qy	408	LENCGAVLLTVVRKGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
Db	416	LENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG	475
Qy	468	IIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD	527
Db	476	IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD	532
Qy	528	HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL	587
Db	533	HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL	592
Qy	588	EFKNDETV	595
Db	593	EFQNDIIV	600

O9TS14

Query Match 66.2%; Score 2136.5; DB 6; Length 941;

RP SEQUENCE FROM N.A.
RC STRAIN=Dahl/Rapp R Sprague-Dawley;
RA Unlap M.T., Bell P.D.;
RT "cDNA cloning of two Na⁺/Ca²⁺ exchangers in mesangial cells from
RT Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF109163; AAD23386.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR004837; NaCa_Exmemb.
DR InterPro; IPR004836; Na_Ca_Ex.
DR Pfam; PF03160; Calx-beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMs; TIGR00845; caca; 1.
DR PROSITE; PS50076; DNAJ_2; 1.
SQ SEQUENCE 934 AA; 104166 MW; C04E0D8A75633DDC CRC64;

Query Match 66.1%; Score 2133; DB 11; Length 934;
Best Local Similarity 67.9%; Pred. No. 6.5e-166;
Matches 424; Conservative 72; Mismatches 88; Indels 40; Gaps 10;

Qy	4	LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK	55
		: : : :	
Db	2	LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK	53
Qy	56	EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFRMASIEVITSQEREVTIK	115
		: : : : : : :	
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFRMSIEVITSQEKEITIK	113
Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAA	175
		: : : : : :	
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIIGICVYVIPDGETRIKIKHLRVFFITAAWSIFAYIWLYMILAVSPGVVQVWEGL	235
		: : : : : : :	
Db	174	FNMFIIIALCVYVVPDGETRIKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL	233
Qy	236	LTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIETEGDHPKG---IEMDGKMM	292
		: : : : : : :	
Db	234	LTFFFFPICVFAWVADRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPASKTEIEMDGKV	293
Qy	293	NSH---FLDGNLVPLEGKEVD-----ESRREMIRILKDLKQKHPEKDLDQLVEMANYALS	345
		: : : : : :	
Db	294	NSHVDNFDLGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qy	346	HQQKSRAFYRIQATRMGTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
		: : : : : : : : : :	
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFEQGT	412
Qy	405	YQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTIVLKPGETQKEF	464
		: : : : : : : : :	
Db	413	YQCLENCGTVALTIIRGGDLTNTVSVDFRTEDGTANAGSDYEFTEGTIVFKPGETQKEI	472

RT "cDNA cloning of two Na⁺/Ca²⁺ exchangers in mesangial cells from
RT Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF109164; AAD23387.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR004837; NaCa_Exmemb.
DR InterPro; IPR004836; Na_Ca_Ex.
DR Pfam; PF03160; Calx-beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMs; TIGR00845; caca; 1.
DR PROSITE; PS50076; DNAJ_2; 1.
SQ SEQUENCE 957 AA; 106724 MW; 7A146630451EAA7E CRC64;

Query Match 66.0%; Score 2129; DB 11; Length 957;
Best Local Similarity 67.8%; Pred. No. 1.4e-165;
Matches 423; Conservative 72; Mismatches 89; Indels 40; Gaps 10;

Qy	4	LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK	55
		: : : :	
Db	2	LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK	53
Qy	56	EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK	115
		: : : : :	
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSIEVITSQEKEITIK	113
Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA	175
		: : : :	
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL	235
		: : : : : :	
Db	174	FNMFIILALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIFLSVSSPGVVEVWEGL	233
Qy	236	LTLEFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKG---IEMDGKMM	292
		: : : : : : :	
Db	234	LTFFFPICVFEAWVADRRLFYKYVYKRYRAGKQKRGMIIEHEGDRPASKTEIEMDGKV	293
Qy	293	NSH---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYALS	345
		: : : :: :	
Db	294	NSHVDNFDLGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qy	346	HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
		: : : : : : :	
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT	412
Qy	405	YQCLENCGAVLLTVVRKGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
		:: : : : : :: : : : : : : : : : :	
Db	413	YQCLENCGTVALTIIRRGDLTNTVSVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qy	465	SVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
		: : : : :	

```

Db      473 RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528
Qy      524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      529 FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588
Qy      584 YGELEFKNDETV-----CDRQE 600
        ||||:||| | ||:|
Db      589 CGELEFONDEIVKIITIRIEDREE 612

```

Q91ZJ7

Query Match 65.9%; Score 2128.5; DB 11; Length 600;
Best Local Similarity 68.7%; Pred. No. 7.8e-166;
Matches 414; Conservative 76; Mismatches 98; Indels 15; Gaps 6;

```

      |::|| ||||| |||||::|||:|||:|||:|||:|||:|||::|
Db      62 EPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPNGETTK 121

Qy      124 TTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIG 183
      ||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      122 TTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIA 181

Qy      184 ICVYVIPDGETRKHRLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFFFPV 243
      :|||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db      182 LCVYVVPDGETRKHRLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEWEGLLTFFFPFI 241

Qy      244 CVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH---FL 297
      ||: ||||:|||||::||| | ||:|| | | | ||||::||| ||
Db      242 CVVFAWVADRLLFYKYVYKRYRAGKQGRMIIEHEGDRPASKTEIEMDGKVVNSHVDNFL 301

Qy      298 DGNLVPLEGKEVD-----ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRF 353
      || || || | | |::||| ||||:|||||:|||::|||:||| || |||||
Db      302 DGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQKSRF 360

Qy      354 YRIQATRMGTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSQCLENCG 412
      |||||::|||:|||:|||:|||:||| || ||: | | :||:|: :|||
Db      361 YRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMEMAENDPVSKIFFEQGTQCLENCG 420

Qy      413 AVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDD 472
      | ||::||:|||:| |::||:||||:||||:|||||: ||||| |||||
Db      421 TVALTIMRRGGDLSTTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEIRVGIIDDD 480

Qy      473 IFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIF 532
      |||||:| | ||||: : |:: : :: | | | ||:| |||||
Db      481 IFEEDENFLVHLSNVRVSSDVSEDGI---LESNHASSIACLGSPSTATITIFDDDHAGIF 537

Qy      533 TFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKND 592
      ||| |||||:|||||:||| ||:||:|:||:||||| ||||:|
Db      538 TFEFPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDTCGELEFQND 597

Qy      593 ETV 595
      | |
Db      598 EIV 600

```

Search completed: June 24, 2004, 16:14:14
Job time : 33.9916 secs

OM protein - protein search, using sw model

Run on: June 24, 2004, 15:55:42 ; Search time 11.6677 Seconds
(without alignments)
2766.900 Million cell updates/sec

Title: US-10-054-680-4
Perfect score: 3228
Sequence: 1 MAWLRLQPLTSAFLHFGLVT.....ADYGRGGQEDSRDGKASIG 620

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	3093	95.8	927	1	NAC3_HUMAN	P57103 homo sapien
2	3016	93.4	927	1	NAC3_RAT	P70549 rattus norv
3	2159.5	66.9	970	1	NAC1_CANFA	P23685 canis famil
4	2152.5	66.7	970	1	NAC1_FELCA	P48767 felis silve
5	2147.5	66.5	970	1	NAC1_BOVIN	P48765 bos taurus
6	2146.5	66.5	973	1	NAC1_HUMAN	P32418 homo sapien
7	2142.5	66.4	970	1	NAC1_CAVPO	P48766 cavia porce
8	2135.5	66.2	971	1	NAC1_RAT	Q01728 rattus norv
9	2115.5	65.5	970	1	NAC1_MOUSE	P70414 mus musculu
10	1961	60.7	921	1	NAC2_HUMAN	Q9upr5 homo sapien
11	1954.5	60.5	921	1	NAC2_RAT	P48768 rattus norv
12	209.5	6.5	663	1	NKX1_CHICK	Q9ial8 gallus gall
13	203.5	6.3	661	1	NKX2_HUMAN	Q9ui40 homo sapien
14	203	6.3	1181	1	NKX1_RAT	Q9qzm6 rattus norv
15	201.5	6.2	670	1	NKX2_RAT	O54701 rattus norv
16	199.5	6.2	651	1	NKX2_CHICK	Q9ial7 gallus gall
17	194.5	6.0	1216	1	NKX1_BOVIN	Q28139 bos taurus

18	193	6.0	605	1	NKX4_HUMAN	Q8nff2	homo sapien
19	189	5.9	605	1	NKX4_MOUSE	Q8cgq8	mus musculu
20	186.5	5.8	644	1	NKX3_HUMAN	Q9hc58	homo sapien
21	181	5.6	624	1	NKX3_RAT	Q9epq0	rattus norv
22	179	5.5	645	1	NKX3_MOUSE	Q99pd7	mus musculu
23	178	5.5	1099	1	NKX1_HUMAN	O60721	homo sapien
24	162.5	5.0	856	1	NCKX_DROME	Q9u6a0	drosophila
25	141.5	4.4	572	1	YKT4_CAEEL	P34315	caenorhabdi
26	132	4.1	1807	1	ITB4_RAT	Q64632	rattus norv
27	131	4.1	590	1	YKTA_CAEEL	P34322	caenorhabdi
28	126.5	3.9	1822	1	ITB4_HUMAN	P16144	homo sapien
29	110	3.4	3358	1	PGCV_MOUSE	Q62059	mus musculu
30	108	3.3	673	1	COAT_PAVBO	P07297	bovine parv
31	107	3.3	548	1	CH60_EHRSE	O32606	ehrlichia s
32	107	3.3	649	1	TOP3_SALTI	Q8z6f5	salmonella
33	106.5	3.3	1036	1	YAN2_SCHPO	Q10068	schizosacch
34	106	3.3	649	1	TOP3_SALTY	P40687	salmonella
35	105.5	3.3	548	1	CH60_EHRRI	P48214	ehrlichia r
36	105	3.3	402	1	PGK_CHLPN	Q9z7m5	chlamydia p
37	104.5	3.2	686	1	MXIA_SHIFL	P35533	shigella fl
38	104.5	3.2	1828	1	MAP2_MOUSE	P20357	mus musculu
39	103.5	3.2	988	1	TNP6_ENTFC	Q06238	enterococcu
40	102.5	3.2	2009	1	CIN1_HUMAN	P35498	homo sapien
41	101.5	3.1	989	1	RPOC_LEUME	P94892	leuconostoc
42	100	3.1	510	1	GPMI_CLOAB	Q97153	clostridium
43	100	3.1	1065	1	SEC8_YEAST	P32855	saccharomyc
44	99.5	3.1	1018	1	SYI_ARCFU	O29622	archaeoglob
45	98.5	3.1	558	1	RTF1_YEAST	P53064	saccharomyc

ALIGNMENTS

RESULT 1

NAC3_HUMAN

ID NAC3_HUMAN STANDARD; PRT; 927 AA.
AC P57103; Q8IUE9; Q8IUF0; Q8NFI7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein
DE 3).
GN SLC8A3 OR NCX3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).
RX MEDLINE=22294016; PubMed=12406570;
RA Gabellini N., Bortoluzzi S., Danieli G.A., Carafoli E.;
RT "The human SLC8A3 gene and the tissue-specific Na⁺/Ca²⁺ exchanger 3
RT isoforms.";
RL Gene 298:1-7(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=22447378; PubMed=12558991;

RA Gabellini N., Bortoluzzi S., Danieli G.A., Carafoli E.;
 RT "Control of the Na⁺/Ca²⁺ exchanger 3 promoter by cyclic adenosine
 RT monophosphate and Ca²⁺ in differentiating neurons."
 RL J. Neurochem. 84:282-293(2003).
 RN [3]
 RP SEQUENCE OF 1-595 FROM N.A.
 RA Kraev A.S., Chumakov I.M., Carafoli E.;
 RT "The organization of the human gene of the sodium-calcium exchanger."
 RL Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores (By similarity).
 CC -!- ENZYME REGULATION: By intracellular calcium ions (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=3; Synonyms=NCX3.3;
 CC IsoId=P57103-1; Sequence=Displayed;
 CC Name=2; Synonyms=NCX3.2;
 CC IsoId=P57103-2; Sequence=VSP_008116;
 CC Name=4; Synonyms=NCX3.4;
 CC IsoId=P57103-3; Sequence=VSP_008117, VSP_008118;
 CC -!- TISSUE SPECIFICITY: Isoform 2 is expressed in brain and skeletal
 CC muscle; Isoform 3 is expressed in excitable cells of brain, retina
 CC and skeletal muscle; Isoform 4 is expressed in skeletal muscle.
 CC -----
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 CC -----
 DR EMBL; AF510501; AAN60790.1; -.
 DR EMBL; AF510502; AAN60791.1; -.
 DR EMBL; AF510503; AAN60792.1; -.
 DR EMBL; AF508982; AAM90955.1; -.
 DR EMBL; X93017; -; NOT_ANNOTATED_CDS.
 DR Genew; HGNC:11070; SLC8A3.
 DR MIM; 607991; -.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 1.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat; Alternative splicing.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 927 SODIUM/CALCIUM EXCHANGER 3.
 FT DOMAIN 31 73 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 74 94 POTENTIAL.
 FT DOMAIN 95 147 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 148 168 POTENTIAL.

FT	DOMAIN	169	169	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	170	190	POTENTIAL.
FT	DOMAIN	191	202	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	203	223	POTENTIAL.
FT	DOMAIN	224	230	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	231	251	POTENTIAL.
FT	DOMAIN	252	726	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	727	747	POTENTIAL.
FT	DOMAIN	748	754	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	755	775	POTENTIAL.
FT	DOMAIN	776	778	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	779	799	POTENTIAL.
FT	DOMAIN	800	828	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	829	849	POTENTIAL.
FT	DOMAIN	850	860	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	861	881	POTENTIAL.
FT	DOMAIN	882	903	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	904	924	POTENTIAL.
FT	DOMAIN	925	927	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	253	272	CALMODULIN-BINDING (BY SIMILARITY).
FT	REPEAT	140	180	ALPHA-1.
FT	REPEAT	399	470	BETA-1.
FT	REPEAT	534	604	BETA-2.
FT	REPEAT	796	832	ALPHA-2.
FT	CARBOHYD	45	45	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	823	823	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	630	635	Missing (in isoform 2).
FT				/FTId=VSP_008116.
FT	VARSPLIC	596	620	KTIRVKIVDEEYERQENFFIALGE -> CDRQEADYGRRG
FT				GQEDSRDGKASIG (in isoform 4).
FT				/FTId=VSP_008117.
FT	VARSPLIC	621	927	Missing (in isoform 4).
FT				/FTId=VSP_008118.
SQ	SEQUENCE	927 AA;	103009 MW;	7B43CB6A9D77615E CRC64;

Query Match 95.8%; Score 3093; DB 1; Length 927;
 Best Local Similarity 100.0%; Pred. No. 6.6e-216;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDKMMNSHFLDGN	300

```

Db      241 FPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qy      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRIFYRIQATR 360
      |||
Db      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRIFYRIQATR 360
Qy      361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      |||
Db      361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Qy      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDHF 480
      |||
Db      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDHF 480
Qy      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
      |||
Db      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qy      541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
      |||
Db      541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

```

RESULT 2

NAC3_RAT

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ID      NAC3_RAT          STANDARD;          PRT;    927 AA.
AC      P70549;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein
DE      3).
GN      SLC8A3 OR NCX3.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Sprague-Dawley; TISSUE=Brain;
RX      MEDLINE=96394663; PubMed=8798769;
RA      Nicoll D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
RA      Philipson K.D.;
RT      "Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.";
RL      J. Biol. Chem. 271:24914-24921(1996).
CC      -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC      coupling. Ca(2+) is extruded from the cell during relaxation so as
CC      to prevent overloading of intracellular stores.
CC      -!- ENZYME REGULATION: By intracellular calcium ions.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -!- TISSUE SPECIFICITY: Expression restricted to brain and skeletal
CC      muscle.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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DR EMBL; U53420; AAC52817.1; -.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR004836; Na_Ca_Ex.
DR InterPro; IPR004837; NaCa_Exmemb.
DR Pfam; PF03160; Calx-beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMs; TIGR00845; caca; 1.
KW Transport; Antiport; Calcium transport; Sodium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW Calmodulin-binding; Repeat.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 927 SODIUM/CALCIUM EXCHANGER 3.
FT DOMAIN 31 73 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 74 94 POTENTIAL.
FT DOMAIN 95 147 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 148 168 POTENTIAL.
FT DOMAIN 169 169 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 170 190 POTENTIAL.
FT DOMAIN 191 202 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 203 223 POTENTIAL.
FT DOMAIN 224 230 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 231 251 POTENTIAL.
FT DOMAIN 252 726 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 727 747 POTENTIAL.
FT DOMAIN 748 754 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 755 775 POTENTIAL.
FT DOMAIN 776 778 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 779 799 POTENTIAL.
FT DOMAIN 800 828 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 829 849 POTENTIAL.
FT DOMAIN 850 860 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 861 881 POTENTIAL.
FT DOMAIN 882 903 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 904 924 POTENTIAL.
FT DOMAIN 925 927 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 253 272 CALMODULIN-BINDING (BY SIMILARITY).
FT REPEAT 140 180 ALPHA-1.
FT REPEAT 399 470 BETA-1.
FT REPEAT 534 604 BETA-2.
FT REPEAT 796 832 ALPHA-2.
FT DOMAIN 645 648 POLY-GLU.
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 823 823 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 927 AA; 103162 MW; EAB35F9620DBE69E CRC64;
  
```

Query Match 93.4%; Score 3016; DB 1; Length 927;
 Best Local Similarity 97.1%; Pred. No. 2.5e-210;
 Matches 578; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MAWLRLQPLTSAFLHFGVLTVFLVFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
 |||

```

Db          1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGDLRDVPSAGQNNESCSGSSDCKEGVIL 60
Qy          61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
          |||
Db          61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Qy          121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180
          |||
Db          121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180
Qy          181 IIGICVYVIPDGETRKKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
          |||:||||:||||
Db          181 IIGICVYVIPDGETRKKIKHLRVFFVTAAWSVFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qy          241 FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
          |||:||||:||||
Db          241 FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIETEGEHPKGIEMDGKMMNSHFLDGN 300
Qy          301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
          |:||||
Db          301 LIPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
Qy          361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
          |||:||||
Db          361 MMTGAGNILKKHAAEQAKKTASMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVR 420
Qy          421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
          |||:||||
Db          421 KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
Qy          481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
          |||:||||
Db          481 FVRLSNVRVEEQLEEGMTPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qy          541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
          |||
Db          541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

```

RESULT 3

NAC1_CANFA

ID NAC1_CANFA STANDARD; PRT; 970 AA.

AC P23685;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).

GN SLC8A1.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RX MEDLINE=91047958; PubMed=1700476;

RA Nicoll D.A., Longoni S., Philipson K.D.;
 RT "Molecular cloning and functional expression of the cardiac
 RT sarcolemmal Na(+)-Ca²⁺ exchanger.";
 RL Science 250:562-565(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=92152737; PubMed=1785844;
 RA Nicoll D.A., Philipson K.D.;
 RT "Molecular studies of the cardiac sarcolemmal sodium-calcium
 RT exchanger.";
 RL Ann. N.Y. Acad. Sci. 639:181-188(1991).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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 DR EMBL; M57523; AAA62766.1; -.
 DR PIR; A36417; A36417.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
 FT DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 POTENTIAL.
 FT DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 168 188 POTENTIAL.
 FT DOMAIN 189 199 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 200 222 POTENTIAL.
 FT DOMAIN 223 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 249 POTENTIAL.
 FT DOMAIN 250 769 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 770 789 POTENTIAL.
 FT DOMAIN 790 796 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 797 819 POTENTIAL.
 FT DOMAIN 820 821 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	822	840	POTENTIAL.
FT	DOMAIN	841	871	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	872	892	POTENTIAL.
FT	DOMAIN	893	903	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	904	924	POTENTIAL.
FT	DOMAIN	925	941	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	942	958	POTENTIAL.
FT	DOMAIN	959	970	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	251	270	CALMODULIN-BINDING (POTENTIAL).
FT	REPEAT	138	178	ALPHA-1.
FT	REPEAT	407	478	BETA-1.
FT	REPEAT	539	609	BETA-2.
FT	REPEAT	839	875	ALPHA-2.
FT	DOMAIN	236	239	POLY-PHE.
FT	DOMAIN	689	692	POLY-GLU.
FT	DOMAIN	756	760	POLY-ASP.
FT	MOD_RES	389	389	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	866	866	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	970 AA;	108004 MW;	BDBCC584846AE08 CRC64;

Query Match 66.9%; Score 2159.5; DB 1; Length 970;
 Best Local Similarity 69.9%; Pred. No. 2.6e-148;
 Matches 425; Conservative 73; Mismatches 89; Indels 21; Gaps 8;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLF--LNLRAEAGSGDVPSTGQNNESCSGSSDCKEGV	58
		: :: : : : :	
Db	1	MLQLRLLPTFSMGCHLLAVVALLFSHVDLISAETEMEGEGNETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN	118
		: :: : :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFGLGVSIADRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM	178
		: : :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFETAGDLGPSTIVGSAAFNM	176
Qy	179	FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL	238
		: : : :	
Db	177	FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH	295
		: : : : : :	
Db	237	FFFPICVVFVAVADRRLLFYKYVYKRYRAGKQRMIIIEHGEDRPSSKTEIEMDGKVVNSH	296
Qy	296	---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ	348
		: : : : : :	
Db	297	VDNFLDGALV-LEVDERDQDDEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355
Qy	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSQC	407
		: : : : : : : : : :	
Db	356	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTQC	415
Qy	408	LENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
		: : : : : : : : : : : : : : : :	
Db	416	LENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG	475

QY 468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
 |||||:| | |||:: | |:| | | | | ||| |||
 Db 476 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---ALACLGSPSTATVTIFDDD 532
 QY 528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
 ||||| | |||||:||||| |||||::|:||||:||||| |||
 Db 533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592
 QY 588 EFKNDETV 595
 ||:| | |
 Db 593 EFQNDEIV 600

RESULT 4

NAC1_FELCA

ID NAC1_FELCA STANDARD; PRT; 970 AA.
 AC P48767; P79174;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
 DE 1).
 GN SLC8A1 OR NCX1.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=96250114; PubMed=8659865;
 RA Menick D.R., Barnes K.V., Thacker U.F., Dawson M.M.,
 RA McDermott D.E., Rozich J.D., Kent R.L., Cooper G.;
 RT "The exchanger and cardiac hypertrophy."
 RL Ann. N.Y. Acad. Sci. 779:489-501(1996).
 RN [2]
 RP SEQUENCE OF 1-600 FROM N.A.
 RX MEDLINE=97269065; PubMed=9111065;
 RA Barnes K.V., Cheng G., Dawson M.M., Menick D.R.;
 RT "Cloning of cardiac, kidney, and brain promoters of the feline ncx1
 RT gene."
 RL J. Biol. Chem. 272:11510-11517(1997).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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```

CC -----
DR EMBL; L35846; AAB41941.1; -.
DR EMBL; U67075; AAB40148.1; -.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR004836; Na_Ca_Ex.
DR InterPro; IPR004837; NaCa_Exmemb.
DR Pfam; PF03160; Calx-beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMs; TIGR00845; caca; 1.
KW Transport; Antiport; Calcium transport; Sodium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW Calmodulin-binding; Repeat.
FT SIGNAL      1      32      POTENTIAL.
FT CHAIN       33     970     SODIUM/CALCIUM EXCHANGER 1.
FT DOMAIN      33      71     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM    72      93     POTENTIAL.
FT DOMAIN      94     133     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   134     155     POTENTIAL.
FT DOMAIN     156     167     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   168     188     POTENTIAL.
FT DOMAIN     189     199     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   200     222     POTENTIAL.
FT DOMAIN     223     225     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   226     249     POTENTIAL.
FT DOMAIN     250     769     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   770     789     POTENTIAL.
FT DOMAIN     790     796     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   797     819     POTENTIAL.
FT DOMAIN     820     821     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   822     840     POTENTIAL.
FT DOMAIN     841     871     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   872     892     POTENTIAL.
FT DOMAIN     893     903     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   904     924     POTENTIAL.
FT DOMAIN     925     941     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   942     958     POTENTIAL.
FT DOMAIN     959     970     CYTOPLASMIC (POTENTIAL).
FT DOMAIN     251     270     CALMODULIN-BINDING (POTENTIAL).
FT REPEAT     138     178     ALPHA-1.
FT REPEAT     407     478     BETA-1.
FT REPEAT     539     609     BETA-2.
FT REPEAT     839     875     ALPHA-2.
FT DOMAIN     236     239     POLY-PHE.
FT DOMAIN     689     692     POLY-GLU.
FT DOMAIN     756     760     POLY-ASP.
FT MOD_RES    389     389     PHOSPHORYLATION (POTENTIAL).
FT CARBOHYD    41      41     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD   157     157     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT    21      21     P -> A (IN REF. 2).
FT CONFLICT   113     113     K -> N (IN REF. 2).
SQ SEQUENCE   970 AA;  108004 MW;  2402F02DE35D4057 CRC64;

```

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Query Match          66.7%; Score 2152.5; DB 1; Length 970;
Best Local Similarity 70.0%; Pred. No. 8.2e-148;
Matches 426; Conservative 72; Mismatches 88; Indels 23; Gaps 10;

```

Qy 1 MAWLRLQPLTSAFLHFGVLTFV-LFLNGLRAEAGGSGDVPSTGQNNES--CSGSSDCKEG 57
| | | | | | | | : | | : : | | | : | | : | | : | | : |
Db 1 MLRLRLSPTFSVGFH--LLAFVPLLFSHVDLI---SADTEMEGEGNETGECTGSYYCKKG 55

Qy 58 VILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKP 117
| | | | | | | : | | | | | | | | | | | | | | | | | | | | | : | | | | | | | |
Db 56 VILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKP 115

Qy 118 NGETSTTTIRVWNETVSNLTIMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAAFN 177
| | | | : | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 116 NGETTKTTVRIWNETVSNLTIMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFN 175

Qy 178 MFIIIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLT 237
| | | | : | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 176 MFIIIALCVYVVPDGETRGIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLT 235

Qy 238 LFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIETEGDHPKG---IEMDGKMMNS 294
| | | | : | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 236 FFFFPICVFAWVADRRLLFYKYVYKRYRAGKQQRGMIEHEGDRPSSKTEIEMDGKVNS 295

Qy 295 H---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLQVEMANYALSHQ 347
| | | | | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 296 HVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQ 354

Qy 348 QKSRAFYRIQATRMGTAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSQ 406
| | | | | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 355 QKSRAFYRIQATRLMTAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTQ 414

Qy 407 CLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSV 466
| | | | | | | | | | | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 415 CLENCGTVALTILRRGGDLTNTVFVDFRTEGTANAGSDYEFTEGTVVFKPGETQKEIRV 474

Qy 467 GIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDD 526
| | | | | | | | | | | | | | : | | | | : | | : | | : | | : | | : | | : | | : | |
Db 475 GIIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDD 531

Qy 527 DHAGIFTFECDTIHVSESIGVMEVKVLRVTSARGTVIVPFRVTEGTAKGGGEDFEDTYGE 586
| | | | | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 532 DHAGIFTFEPPVTHVSESIGIMEVKVLRVTSARGNVIVPYKTIEGTARGGGEDFEDTCGE 591

Qy 587 LEFKNDETV 595
| | | : | | | |
Db 592 LEFQNDIV 600

RESULT 5

NAC1_BOVIN

ID NAC1_BOVIN STANDARD; PRT; 970 AA.

AC P48765;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).

GN SLC8A1.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=93037494; PubMed=1416984;
 RA Aceto J.F., Condrescu M., Kroupis C., Nelson H., Nelson N.,
 RA Nicoll D.A., Philipson K.D., Reeves J.P.;
 RT "Cloning and expression of the bovine cardiac sodium-calcium
 RT exchanger.";
 RL Arch. Biochem. Biophys. 298:553-560(1992).
 RN [2]
 RP SUBCELLULAR LOCATION.
 RC TISSUE=Retinal rod cell;
 RX MEDLINE=90241959; PubMed=2334719;
 RA Reid D.M., Friedel U., Molday R.S., Cook N.J.;
 RT "Identification of the sodium-calcium exchanger as the major
 RT ricin-binding glycoprotein of bovine rod outer segments and its
 RT localization to the plasma membrane.";
 RL Biochemistry 29:1601-1607(1990).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.

CC -----
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 CC -----

DR EMBL; L06438; AAA30509.1; -.
 DR PIR; S27114; S27114.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
 FT DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 POTENTIAL.
 FT DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	168	188	POTENTIAL.
FT	DOMAIN	189	199	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	200	222	POTENTIAL.
FT	DOMAIN	223	225	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	226	249	POTENTIAL.
FT	DOMAIN	250	769	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	770	789	POTENTIAL.
FT	DOMAIN	790	796	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	797	819	POTENTIAL.
FT	DOMAIN	820	821	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	822	840	POTENTIAL.
FT	DOMAIN	841	871	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	872	892	POTENTIAL.
FT	DOMAIN	893	903	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	904	924	POTENTIAL.
FT	DOMAIN	925	941	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	942	958	POTENTIAL.
FT	DOMAIN	959	970	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	251	270	CALMODULIN-BINDING (POTENTIAL).
FT	REPEAT	138	178	ALPHA-1.
FT	REPEAT	407	478	BETA-1.
FT	REPEAT	539	609	BETA-2.
FT	REPEAT	839	875	ALPHA-2.
FT	DOMAIN	236	239	POLY-PHE.
FT	DOMAIN	689	692	POLY-GLU.
FT	DOMAIN	756	760	POLY-ASP.
FT	MOD_RES	389	389	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	866	866	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	970 AA;	108027 MW;	7C29153D1F87DDBE CRC64;

Query Match 66.5%; Score 2147.5; DB 1; Length 970;
 Best Local Similarity 69.4%; Pred. No. 1.9e-147;
 Matches 422; Conservative 74; Mismatches 91; Indels 21; Gaps 8;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLF--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV	58
		: : : : : : :	
Db	1	MLQFSLSPTLSMGFHVIAVALLFSHVDHISAETEMEGEGNETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN	118
		: : : : : : : :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNM	178
		: : : : : : : : :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM	176
Qy	179	FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL	238
		: : : : : : :	
Db	177	FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH	295
		: : : : : : : : : :	
Db	237	FFFPICVFAWVADRLLFYKYVYKRYRAGKQGRGMIIEHEGDRPSSKTEIEMDGKVNSH	296
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQLVEMANYYALSHQQ	348

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      |||| || || | | | :||| |||:|||||::||:|:| | || ||
Db      297 VDSFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355

Qy      349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
      |||||:|||||:||||:| | ||:| | :||:|: :|||
Db      356 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTQC 415

Qy      408 LENC GAVLLTVVRKGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
      |||| | ||::|:|:|: |::|:|:|:|:|:|:|:|:| | || || ||
Db      416 LENC GTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

Qy      468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
      |||||:| | |||:| | :|:| | | | | || || || || ||
Db      476 IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVS---TLACLGSPSTATVTIFDDD 532

Qy      528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
      ||||| | |||||:||||| | |||:|:|:|:|:|:| | || ||
Db      533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy      588 EFKNDETV 595
      ||:| | |
Db      593 EFQNDEIV 600

```

RESULT 6

NAC1_HUMAN

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ID      NAC1_HUMAN      STANDARD;      PRT;      973 AA.
AC      P32418; O95849; Q9UBL8; Q9UDN1; Q9UDN2; Q9UKX6;
DT      01-OCT-1993 (Rel. 27, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
DE      1).
GN      SLC8A1 OR NCX1 OR CNC.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM 1).
RC      TISSUE=Heart;
RX      MEDLINE=92262521; PubMed=1374913;
RA      Komuro I., Wenninger K.E., Philipson K.D., Izumo S.;
RT      "Molecular cloning and characterization of the human cardiac Na+/Ca2+
RT      exchanger cDNA.";
RL      Proc. Natl. Acad. Sci. U.S.A. 89:4769-4773(1992).
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORMS 3 AND 7).
RX      MEDLINE=21136211; PubMed=11241183;
RA      Van Eylen F., Bollen A., Herchuelz A.;
RT      "NCX1 Na/Ca exchanger splice variants in pancreatic islet cells.";
RL      J. Endocrinol. 168:517-526(2001).
RN      [3]
RP      SEQUENCE FROM N.A. (ISOFORM 7).
RA      Mangini N.J., Chen W., Wang Q., Kennedy B.G.;
RT      "Na+/Ca2+ exchanger isoforms in cultured human retinal pigment
RT      epithelium.";

```

RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE OF 1-603 FROM N.A.
 RA Rohlfing T., Strowmatt C., Scronce D., Moody T.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE OF 850-973 FROM N.A.
 RA Kozlowicz A., Stoneking T., Hawkins M., Le T.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE OF 459-681 FROM N.A. (ISOFORM 10).
 RA Lundquist P., Lundgren T., Gritli-Linde A., Linde A.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1; Synonyms=NaCa1, NCX1.1;
 CC IsoId=P32418-1; Sequence=Displayed;
 CC Name=3; Synonyms=NaCa3, NCX1.3;
 CC IsoId=P32418-2; Sequence=VSP_003397, VSP_003398, VSP_003400;
 CC Name=7; Synonyms=NaCa7, NCX1.7;
 CC IsoId=P32418-3; Sequence=VSP_003397, VSP_003398, VSP_003399;
 CC Name=10; Synonyms=NaCa10, NCX1.10;
 CC IsoId=P32418-4; Sequence=VSP_003397, VSP_003398;
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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 CC -----
 DR EMBL; M91368; AAA35702.1; -.
 DR EMBL; AF108388; AAF08987.1; -.
 DR EMBL; AF108389; AAF08988.1; -.
 DR EMBL; AF128524; AAD26362.1; -.
 DR EMBL; AC007281; AAF19237.1; -.
 DR EMBL; AC007254; AAF19235.1; -.
 DR EMBL; AF115505; AAD17213.1; -.
 DR PIR; S32815; S32815.
 DR Genew; HGNC:11068; SLC8A1.
 DR MIM; 182305; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0015085; F:calcium ion transporter activity; TAS.
 DR GO; GO:0015081; F:sodium ion transporter activity; TAS.
 DR GO; GO:0006816; P:calcium ion transport; TAS.
 DR GO; GO:0006936; P:muscle contraction; TAS.
 DR GO; GO:0006814; P:sodium ion transport; TAS.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.

DR	InterPro; IPR004837; NaCa_Exmemb.			
DR	Pfam; PF03160; Calx-beta; 2.			
DR	Pfam; PF01699; Na_Ca_Ex; 2.			
DR	PRINTS; PR01259; NACAEXCHNGR.			
DR	SMART; SM00237; Calx_beta; 2.			
DR	TIGRFAMs; TIGR00845; caca; 1.			
KW	Transport; Antiport; Calcium transport; Sodium transport;			
KW	Transmembrane; Glycoprotein; Phosphorylation; Signal;			
KW	Calmodulin-binding; Repeat; Alternative splicing; Polymorphism.			
FT	SIGNAL	1	35	POTENTIAL.
FT	CHAIN	36	973	SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN	36	74	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	75	96	POTENTIAL.
FT	DOMAIN	97	136	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	137	158	POTENTIAL.
FT	DOMAIN	159	170	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	171	191	POTENTIAL.
FT	DOMAIN	192	202	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	203	225	POTENTIAL.
FT	DOMAIN	226	228	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	229	252	POTENTIAL.
FT	DOMAIN	253	772	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	773	792	POTENTIAL.
FT	DOMAIN	793	799	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	800	822	POTENTIAL.
FT	DOMAIN	823	824	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	825	843	POTENTIAL.
FT	DOMAIN	844	874	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	875	895	POTENTIAL.
FT	DOMAIN	896	906	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	907	927	POTENTIAL.
FT	DOMAIN	928	944	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	945	961	POTENTIAL.
FT	DOMAIN	962	973	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	254	273	CALMODULIN-BINDING (POTENTIAL).
FT	REPEAT	141	181	ALPHA-1.
FT	REPEAT	410	481	BETA-1.
FT	REPEAT	542	612	BETA-2.
FT	REPEAT	842	878	ALPHA-2.
FT	DOMAIN	239	242	POLY-PHE.
FT	DOMAIN	692	695	POLY-GLU.
FT	DOMAIN	759	763	POLY-ASP.
FT	MOD_RES	392	392	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	44	44	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	160	160	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	869	869	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	605	613	TISVKVIDD -> IITIRIFDR (in isoform 3,
FT				isoform 7 and isoform 10).
FT				/FTId=VSP_003397.
FT	VARSPPLIC	619	645	NKTFEIGEPRLVEMSEKKALLNEL -> ECSFSLVLEE
FT				PKWIRRGMK (in isoform 3, isoform 7 and
FT				isoform 10).
FT				/FTId=VSP_003398.
FT	VARSPPLIC	652	656	Missing (in isoform 7).
FT				/FTId=VSP_003399.
FT	VARSPPLIC	652	679	Missing (in isoform 3).
FT				/FTId=VSP_003400.

Query Match 66.5%; Score 2146.5; DB 1; Length 973;
Best Local Similarity 69.2%; Pred. No. 2.2e-147;
Matches 421; Conservative 76; Mismatches 90; Indels 21; Gaps 8;

```

RESULT 7
NAC1_CAVPO
ID   NAC1_CAVPO      STANDARD;          PRT;    970 AA.
AC   P48766;

```

DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
 DE 1).
 GN SLC8A1.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=95078257; PubMed=7986817;
 RA Tsuruya Y., Bersohn M.M., Li Z., Nicoll D.A., Philipson K.D.;
 RT "Molecular cloning and functional expression of the guinea pig
 RT cardiac Na(+)-Ca2+ exchanger.";
 RL Biochim. Biophys. Acta 1196:97-99(1994).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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 CC -----
 DR EMBL; U04955; AAA73904.1; -.
 DR PIR; I48097; I48097.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
 FT DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 POTENTIAL.
 FT DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 168 188 POTENTIAL.
 FT DOMAIN 189 199 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 200 222 POTENTIAL.
 FT DOMAIN 223 225 EXTRACELLULAR (POTENTIAL).

RN [4]
 RP TISSUE SPECIFICITY.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96394663; PubMed=8798769;
 RA Nicoll D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
 RA Philipson K.D.;
 RT "Cloning of a third mammalian Na⁺-Ca²⁺ exchanger, NCX3."
 RL J. Biol. Chem. 271:24914-24921(1996).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=1; Synonyms=Heart, NaCa1;
 CC IsoId=Q01728-1; Sequence=Displayed;
 CC Name=2; Synonyms=Brain-1, NaCa5;
 CC IsoId=Q01728-2; Sequence=VSP_003402, VSP_003403;
 CC Name=3; Synonyms=Brain-2, NaCa4;
 CC IsoId=Q01728-3; Sequence=VSP_003402, VSP_003404;
 CC Name=4; Synonyms=Kidney-1, NaCa7;
 CC IsoId=Q01728-4; Sequence=VSP_003401, VSP_003402, VSP_003403;
 CC Name=5; Synonyms=Kidney-2, NaCa3;
 CC IsoId=Q01728-5; Sequence=VSP_003401, VSP_003402, VSP_003404;
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma or brain, and spleen.
 CC -----
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 CC -----
 DR EMBL; X68191; CAA48273.1; -.
 DR EMBL; X68812; CAA48707.1; -.
 DR EMBL; X68813; CAA48708.1; -.
 DR EMBL; U04933; AAB39952.1; -.
 DR EMBL; U04934; AAA19124.1; -.
 DR EMBL; U04936; AAA19125.1; -.
 DR PIR; A53789; A53789.
 DR PIR; S28833; S28833.
 DR PIR; S32435; S32435.
 DR PIR; S43730; S43730.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat; Alternative splicing.
 FT SIGNAL 1 32 POTENTIAL.

FT	CHAIN	33	971	SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN	33	71	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	72	93	POTENTIAL.
FT	DOMAIN	94	133	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	134	155	POTENTIAL.
FT	DOMAIN	156	167	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	168	188	POTENTIAL.
FT	DOMAIN	189	199	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	200	222	POTENTIAL.
FT	DOMAIN	223	225	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	226	249	POTENTIAL.
FT	DOMAIN	250	770	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	771	790	POTENTIAL.
FT	DOMAIN	791	797	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	798	820	POTENTIAL.
FT	DOMAIN	821	822	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	823	841	POTENTIAL.
FT	DOMAIN	842	872	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	873	893	POTENTIAL.
FT	DOMAIN	894	904	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	905	925	POTENTIAL.
FT	DOMAIN	926	942	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	943	959	POTENTIAL.
FT	DOMAIN	960	971	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	251	270	CALMODULIN-BINDING (BY SIMILARITY).
FT	REPEAT	138	178	ALPHA-1.
FT	REPEAT	407	478	BETA-1.
FT	REPEAT	539	609	BETA-2.
FT	REPEAT	840	876	ALPHA-2.
FT	DOMAIN	236	239	POLY-PHE.
FT	DOMAIN	690	693	POLY-GLU.
FT	DOMAIN	757	761	POLY-ASP.
FT	MOD_RES	389	389	PHOSPHORYLATION (BY SIMILARITY).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	867	867	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	602	635	TISVKVIDDEEYEKNTFFIEIGEPRLVEMSEKK -> IIT
FT				IRIFDREEYEKECSFSLVLEEPKWIRRGMK (in
FT				isoform 4 and isoform 5).
FT				/FTid=VSP_003401.
FT	VARSPPLIC	636	642	Missing (in isoform 2, isoform 3, isoform
FT				4 and isoform 5).
FT				/FTid=VSP_003402.
FT	VARSPPLIC	649	654	Missing (in isoform 2 and isoform 4).
FT				/FTid=VSP_003403.
FT	VARSPPLIC	649	677	Missing (in isoform 3 and isoform 5).
FT				/FTid=VSP_003404.
FT	CONFLICT	250	250	D -> A (IN REF. 1).
FT	CONFLICT	402	402	P -> A (IN REF. 1).
SQ	SEQUENCE	971 AA;	108184 MW;	EC456CFE3AFC6A69 CRC64;

Query Match 66.2%; Score 2135.5; DB 1; Length 971;
 Best Local Similarity 68.8%; Pred. No. 1.4e-146;
 Matches 421; Conservative 72; Mismatches 86; Indels 33; Gaps 9;

Qy 4 LRLQPLTSAFLHFGVLTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK 55
 ||| : : | ||| | | || ||: |: || ||

Db 2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53

Qy 56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
:||||| |:| | ||||| |||||:||||||| |:| |

Db 54 KGVILPIWEPQDPSEFGDKIARATVYFVAMVYMFVGVSIIADRFMSSIEVITSQEKEITIK 113

Qy 116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCVGHGFIAGDLGPSTIVGSAA 175
|||||: |:|:||||||| |||||:||||| | |||||

Db 114 KPNGETTKTVRIWNETVSNLTLMALGSSAPEILLSVIEVCVGHNFTAGDLGPSTIVGSAA 173

Qy 176 FNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEG 235
|||||: |:|:||||||| |||||:||||| ||:|:| |||||:|||||

Db 174 FNMFIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEG 233

Qy 236 LTLFFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKG---IEMDGKMM 292
|| |:|:| |:|:| |:|:| |:|:| | |:| | | |:|:|

Db 234 LTLFFFFPICVVFVAVDRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPASKTEIEMDGKVV 293

Qy 293 NSH---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQVEMANYALS 345
|| | | | | | | | | | |:| | |:| | |:| | |:| | | |

Db 294 NSHVDNFLDGLV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS 352

Qy 346 HQQKSRFYRIQATRMGTGAGNILLKHAEEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
||||||| |:| | |:|:| |:|:| | | |:| | | |:| | |

Db 353 QQQKSRFYRIQATRLMTGAGNILLKHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412

Qy 405 YQCLENCGAVLLTVVRKGGMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
||||||| | |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |

Db 413 YQCLENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472

Qy 465 SVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
||||||| |:| | |:|:| | |:| | |:| | |:| | |:| |

Db 473 RVGIIDDDIFEEDENFLVHLSNVRSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528

Qy 524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
||||||| | |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |

Db 529 FDDDHAGIFTFEEPVTIHVSESIGIMEVKVLRITSGARGNVIIPYKTIEGTARGGGGEDFEDT 588

Qy 584 YGELEFKNDETV 595
||||:| |

Db 589 CGELEFQNDIV 600

RESULT 9

NAC1_MOUSE

ID NAC1_MOUSE STANDARD; PRT; 970 AA.

AC P70414;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein

DE 1).

GN SLC8A1 OR NCX.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=96250070; PubMed=8659820;
 RA Kim I., Lee C.O.;
 RT "Cloning of the mouse cardiac Na(+)-Ca2+ exchanger and functional
 RT expression in Xenopus oocytes."
 RL Ann. N.Y. Acad. Sci. 779:126-128(1996).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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 CC -----
 DR EMBL; U70033; AAB46708.1; -.
 DR MGD; MGI:107956; Slc8a1.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMS; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
 FT DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 POTENTIAL.
 FT DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 168 188 POTENTIAL.
 FT DOMAIN 189 199 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 200 222 POTENTIAL.
 FT DOMAIN 223 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 249 POTENTIAL.
 FT DOMAIN 250 769 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 770 789 POTENTIAL.
 FT DOMAIN 790 796 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 797 819 POTENTIAL.
 FT DOMAIN 820 821 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 822 840 POTENTIAL.
 FT DOMAIN 841 871 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 872 892 POTENTIAL.
 FT DOMAIN 893 903 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	904	924	POTENTIAL.
FT	DOMAIN	925	941	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	942	958	POTENTIAL.
FT	DOMAIN	959	970	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	251	270	CALMODULIN-BINDING (POTENTIAL).
FT	REPEAT	138	178	ALPHA-1.
FT	REPEAT	407	478	BETA-1.
FT	REPEAT	539	609	BETA-2.
FT	REPEAT	839	875	ALPHA-2.
FT	DOMAIN	236	239	POLY-PHE.
FT	DOMAIN	689	692	POLY-GLU.
FT	DOMAIN	756	760	POLY-ASP.
FT	MOD_RES	389	389	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	866	866	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	970 AA;	108035 MW;	F5FC0BD07F2B6602 CRC64;

Query Match 65.5%; Score 2115.5; DB 1; Length 970;
 Best Local Similarity 68.3%; Pred. No. 3.9e-145;
 Matches 412; Conservative 76; Mismatches 100; Indels 15; Gaps 6;

Qy	4	LRLQPLTSAFLHFGVLTVFLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIW	63
		: : : : : :	
Db	2	LRLSLPPNVSMGFRLVALVALLFSHVDHITADTEAETGGNETTECTGSYYCKKGVLPIW	61
Qy	64	YPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGETST	123
		: : : : :	
Db	62	EPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPNGETTK	121
Qy	124	TTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIG	183
		: : : : :	
Db	122	TTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIA	181
Qy	184	ICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFFFPV	243
		: : : : : : :	
Db	182	LCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTFFFFP	241
Qy	244	CVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH---FL	297
		: : : : : :	
Db	242	CVVFAWVADRRLLFYKYVKRYRAGKQGMIIIEHEDRPASKTEIEMDGKVNSHVDNFL	301
Qy	298	DGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLQVLVEMANYALSHQQKSR	353
		: : : :	
Db	302	DGALV-LEVDERDQDDEEARREMARILKELQKHPEKEIEQLIELANYQVLSQQQKSR	360
Qy	354	YRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLENC	412
		: : : : : : : : :	
Db	361	YRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMEMAENDPVSKIFFEQGTQYQCLENC	420
Qy	413	AVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDD	472
		: : : : : : : : : : : :	
Db	421	TVALTIMRRGGDLSTTVFVDFERTEDGTANAASDYEFTEGTVIFKPGETQKEIRVGIIDD	480
Qy	473	IFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIF	532
		: : : : : : :	
Db	481	IFEEDENFLVHLSNVRVSSDVSEDGI---LESNHASSIACLGSPSTATITIFDDDHAGIF	537

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Qy      533 TFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKND 592
      ||| |||||:||||||| ||:|::|:||||| || ||:|
Db      538 TFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDTCGEPEFQND 597

Qy      593 ETV 595
      | |
Db      598 EIV 600

```

RESULT 10

NAC2_HUMAN

```

ID      NAC2_HUMAN      STANDARD;      PRT;      921 AA.
AC      Q9UPR5;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein
DE      2).
GN      SLC8A2 OR NCX2 OR KIAA1087.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=99397452; PubMed=10470851;
RA      Kikuno R., Nagase T., Ishikawa K.-I., Hirose M., Miyajima N.,
RA      Tanaka A., Kotani H., Nomura N., Ohara O.;
RT      "Prediction of the coding sequences of unidentified human genes. XIV.
RT      The complete sequences of 100 new cDNA clones from brain which code
RT      for large proteins in vitro.";
RL      DNA Res. 6:197-205(1999).
CC      -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC      coupling. Ca(2+) is extruded from the cell during relaxation so as
CC      to prevent overloading of intracellular stores (By similarity).
CC      -!- ENZYME REGULATION: By ATP (By similarity).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AB029010; BAA83039.1; ALT_INIT.
DR      Genew; HGNC:11069; SLC8A2.
DR      MIM; 601901; -.
DR      InterPro; IPR003644; Calx_beta.
DR      InterPro; IPR004836; Na_Ca_Ex.
DR      InterPro; IPR004837; NaCa_Exmemb.
DR      Pfam; PF03160; Calx-beta; 2.
DR      Pfam; PF01699; Na_Ca_Ex; 2.
DR      PRINTS; PR01259; NACAEXCHNGR.

```


RA Philipson K.D.;
 RT "Cloning of a third mammalian Na⁺-Ca²⁺ exchanger, NCX3.";
 RL J. Biol. Chem. 271:24914-24921(1996).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Brain and skeletal muscle.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U08141; AAA19920.1; -.
 DR PIR; A54139; A54139.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 921 SODIUM/CALCIUM EXCHANGER 2.
 FT DOMAIN 21 68 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 69 90 POTENTIAL.
 FT DOMAIN 91 130 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 131 152 POTENTIAL.
 FT DOMAIN 153 164 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 165 185 POTENTIAL.
 FT DOMAIN 186 196 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 197 219 POTENTIAL.
 FT DOMAIN 220 222 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 223 246 POTENTIAL.
 FT DOMAIN 247 720 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 721 740 POTENTIAL.
 FT DOMAIN 741 747 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 748 770 POTENTIAL.
 FT DOMAIN 771 772 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 773 791 POTENTIAL.
 FT DOMAIN 792 822 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 823 843 POTENTIAL.
 FT DOMAIN 844 854 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 855 875 POTENTIAL.
 FT DOMAIN 876 892 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 893 909 POTENTIAL.
 FT DOMAIN 910 921 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 248 267 CALMODULIN-BINDING (BY SIMILARITY).

Query Match 60.5%; Score 1954.5; DB 1; Length 921;
Best Local Similarity 64.1%; Pred. No. 1.6e-133;
Matches 371; Conservative 92; Mismatches 91; Indels 25; Gaps 6;

Qy	31	EAGGSGDVPSTGQNE-----SCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALI	85
		: : : : : : : :	
Db	21	EATPTPSLPPPPANDSDASPGGCQGSYRCQPGVLLPWWEPDDPSLGDKAARAVVYFVAMV	80
Qy	86	YMFLGVSIIADRFMASIEVITSQEREVTIKPNGETSTTTIRVWNETVSNLTLMALGSSA	145
		: : :	
Db	81	YMFLGLSIIADRFMASIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSA	140
Qy	146	PEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKHKLRVFFI	205
		: : : :	
Db	141	PEILLSVIEVCGHNFQAGELGPGTIVGSAAFNMFVIIACVYVIPAGESRKIKHLRVFFV	200
Qy	206	TAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLLLLFPVCVLLAWVADKRLLFYKYMHKKY	265
		: : : : : :	
Db	201	TASWSIFAYVWLYLILAVFSPGVVQVWEALLTLVFFPVCVFPAWMADKRLLFYKYVKRY	260
Qy	266	RTDKHRGIIIETEGDHPKGIEMDGKMNSHFLDGNL-----VPLEGKEVDSESRREMIRIL	320
		: :	
Db	261	RTDPRSGIIIGAEGDPKSIELDGTFTVGTE-VPGEGLGALGTGPAEARELDASRREVIQIL	319
Qy	321	KDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKA	380
		: : : : : : : :	
Db	320	KDLKQKHDPKDLEQLVGIAKYYALLHQKSRAFYRIQATRLMTGAGNVLRRAADAARRP	379
Qy	381	SSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGMDSKTMVVDYKTEDGSA	440
		: : : : : : : : : : :	
Db	380	GA-NDGAPDDEDGASRIFFEPSLYHCLENCGSVLLSVACQGEGNSTFYVDYRTEDGSA	438
Qy	441	NAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDHEHFFVRLSNVRIEEEQ----PEE	496
		: : :	
Db	439	KAGSDYEYSEGTLVFKPGETQKELRIGIIDDDIFEEDHEHFFVRLNLNRVGDAQGMFEPDG	498
Qy	497	GMPPAIFNSLPLPRAVLASPCVATVTILDDD HAGIFTFECDTIHVSESIGVMEVKVLRTS	556
		: : : : : : : :	
Db	499	G-----GRPKGRLVAPLLATVTILDDD HAGIFS QDRLLHVSECMTVDVRVVRSS	549
Qy	557	GARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET V	595
		: : : : : : :	
Db	550	GARGTVRLPYRTVDGTARGGGVHYEDACGELEFGDDETM	588

RESULT 12
NKX1 CHICK

ID NKX1_CHICK STANDARD; PRT; 663 AA.
AC Q9IAL8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-
DE exchange protein 1) (Retinal rod Na-Ca+K exchanger).
GN SLC24A1 OR NCKX1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=20130359; PubMed=10662833;
RA Prinsen C.F.M., Szerencsei R.T., Schnetkamp P.P.M.;
RT "Molecular cloning and functional expression of the potassium-
RT dependent sodium-calcium exchanger from human and chicken retinal cone
RT photoreceptors.";
RL J. Neurosci. 20:1424-1434(2000).
CC -!- FUNCTION: Critical component of the visual transduction cascade,
CC controlling the calcium concentration of outer segments during
CC light and darkness. Light causes a rapid lowering of cytosolic
CC free calcium in the outer segment of both retinal rod and cone
CC photoreceptors and the light-induced lowering of calcium is caused
CC by extrusion via this protein which plays a key role in the
CC process of light adaptation. Transports one Ca(2+) and one K(+) in
CC exchange for four Na(+).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Retinal rods. Localizes to the inner segment
CC of rod photoreceptors.
CC -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF177984; AAF25808.1; -.
DR InterPro; IPR004817; K_NaCaexchang.
DR InterPro; IPR004481; K_NaCaexchnng.
DR InterPro; IPR004837; NaCa_Exmemb.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR TIGRFAMs; TIGR00927; 2A1904; 1.
DR TIGRFAMs; TIGR00367; TIGR00367; 1.
KW Vision; Transport; Antiport; Symport; Calcium transport;
KW Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
KW Phosphorylation; Signal; Repeat.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 663 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
FT DOMAIN 32 128 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 129 149 POTENTIAL.

FT	DOMAIN	150	173	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	174	194	POTENTIAL.
FT	DOMAIN	195	200	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	201	221	POTENTIAL.
FT	DOMAIN	222	228	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	229	253	POTENTIAL.
FT	DOMAIN	254	259	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	260	276	POTENTIAL.
FT	DOMAIN	277	471	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	472	492	POTENTIAL.
FT	DOMAIN	493	499	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	500	520	POTENTIAL.
FT	DOMAIN	521	535	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	536	556	POTENTIAL.
FT	DOMAIN	557	574	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	575	595	POTENTIAL.
FT	DOMAIN	596	604	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	605	625	POTENTIAL.
FT	DOMAIN	626	632	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	633	653	POTENTIAL.
FT	DOMAIN	654	663	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	170	210	ALPHA-1.
FT	REPEAT	543	574	ALPHA-2.
FT	MOD_RES	337	337	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	59	59	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	66	66	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	100	100	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	663 AA;	73771 MW;	DD624E3080C43082 CRC64;

Query Match 6.5%; Score 209.5; DB 1; Length 663;
 Best Local Similarity 21.9%; Pred. No. 2.1e-07;
 Matches 124; Conservative 74; Mismatches 166; Indels 203; Gaps 26;

Qy	77	VIVYFVALIYMFLGVSIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN	135
		::: :: :: : :: : :: :: :	::: :: :
Db	131	VVLHIFGMMYVFVALAIVCDEYFVPALGVITEK-----LQI-SEDVAG	172
Qy	136	LTLMALGSSAPEILLSLIEVCGHGFA-GDLGPSTIVGSAAFNMFIIGICVYVIPDGET	194
		: : :: : :: :	:
Db	173	ATFMAAGGSAPELFTSLIGV----FISHSNVGIGTIVGSAVFNILFVIGTCALF-----S	223
Qy	195	RKIKHLRVFFITAAWSIFAYIWLY-----MILAVFSPGVVQVWEGLLTLFFFPVCV----	245
		: : :: : :	
Db	224	REILHL-----TWWPLFRDISFYIVDLLMLILFFLDSDVIDWWESLLLLTAYATYVFTMK	277
Qy	246	----LLAWVADK-----RLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMM-	292
		:: : :: : : : :	
Db	278	HNVSLEQWVKEELSKKLNAVQAASAEHMRKK-----SSVAVAEDGTKP----ADGKKLQ	327
Qy	293	-----NS-----HFLDGNLVPLEGKEVDESRRMIRILKDLKQK	326
		: :: : :: :	
Db	328	PTTALQRGTTSSASLHNSQMRSTIFQLMIHTLD----PLAGAKF----KDRV DILSNI AKV	379
Qy	327	HPEKDLDLQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEV	386
		: : :	
Db	380	KADS-----LTGQGT---KPEAEEEKQASQ----	401


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Qy      387 HTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGMSKTMVVDYKTEDGSANAGADY 446
          : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      402 -----NTVQVTPAS-----DSEPSKDKQKEDTPQDGQPPSDSD- 434

Qy      447 EFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSL 506
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      435 -----NSEDSSSDSEDDSDDDSTDDEE-----NDEPLSLEWPETRKKQAIYLF 478

Qy      507 PLPRAVLASPCVATVTIL---DDDHAGIFTFECDTI-----HVSESIGVME 549
          | : | : | : | : | | | | | | | | | | | | | | | |
Db      479 -FP---IVFPLWSTIPDVRNPDSKKFFVITFFGSIIWIAAFSYLMVWWAHQVGETIGISE 534

Qy      550 VKVLRRTSGARGTVIVPFRTVEGTAKGG 576
          : | | | | | | | | | | | | | | | | | | | | | |
Db      535 EIMGLTILAAGTSIPDLITSVIVARKG 561

```

RESULT 13

NKX2_HUMAN

```

ID      NKX2_HUMAN      STANDARD;      PRT;      661 AA.
AC      Q9UI40; Q9NTN5; Q9NZQ4;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Sodium/potassium/calcium exchanger 2 precursor (Na(+)/K(+)/Ca(2+)-
DE      exchange protein 2) (Retinal cone Na-Ca+K exchanger).
GN      SLC24A2 OR NCKX2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC      TISSUE=Retina;
RX      MEDLINE=20130359; PubMed=10662833;
RA      Prinsen C.F.M., Szerencsei R.T., Schnetkamp P.P.M.;
RT      "Molecular cloning and functional expression of the potassium-
RT      dependent sodium-calcium exchanger from human and chicken retinal cone
RT      photoreceptors.";
RL      J. Neurosci. 20:1424-1434(2000).
RN      [2]
RP      SEQUENCE OF 311-376 FROM N.A. (ISOFORM 1).
RA      Sehra H.;
RL      Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC      -!- FUNCTION: Critical component of the visual transduction cascade,
CC      controlling the calcium concentration of outer segments during
CC      light and darkness. Light causes a rapid lowering of cytosolic
CC      free calcium in the outer segment of both retinal rod and cone
CC      photoreceptors and the light-induced lowering of calcium is caused
CC      by extrusion via this protein which plays a key role in the
CC      process of light adaptation. Transports one Ca(2+) and one K(+) in
CC      exchange for four Na(+).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      IsoId=Q9UI40-1; Sequence=Displayed;

```

```

CC      Name=2;
CC      IsoId=Q9UI40-2; Sequence=VSP_006164;
CC      -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF097366; AAF21810.1; -.
DR      EMBL; AF177987; AAF25811.1; -.
DR      EMBL; AL133281; CAB92751.2; -.
DR      Genew; HGNC:10976; SLC24A2.
DR      InterPro; IPR004481; K_NaCaexchnng.
DR      InterPro; IPR004837; NaCa_Exmemb.
DR      Pfam; PF01699; Na_Ca_Ex; 2.
DR      TIGRFAMs; TIGR00367; TIGR00367; 1.
KW      Vision; Transport; Antiport; Symport; Calcium transport;
KW      Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
KW      Signal; Repeat; Alternative splicing.
FT      SIGNAL      1      58      POTENTIAL.
FT      CHAIN      59      661      SODIUM/POTASSIUM/CALCIUM EXCHANGER 2.
FT      DOMAIN      59      132      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      133      153      POTENTIAL.
FT      DOMAIN      154      178      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      179      199      POTENTIAL.
FT      DOMAIN      200      204      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      205      225      POTENTIAL.
FT      DOMAIN      226      243      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      244      264      POTENTIAL.
FT      DOMAIN      265      265      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      266      286      POTENTIAL.
FT      DOMAIN      287      469      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      470      490      POTENTIAL.
FT      DOMAIN      491      497      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      498      518      POTENTIAL.
FT      DOMAIN      519      533      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      534      554      POTENTIAL.
FT      DOMAIN      555      569      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      570      590      POTENTIAL.
FT      DOMAIN      591      602      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      603      623      POTENTIAL.
FT      DOMAIN      624      630      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      631      651      POTENTIAL.
FT      DOMAIN      652      661      CYTOPLASMIC (POTENTIAL).
FT      REPEAT      174      214      ALPHA-1.
FT      REPEAT      541      572      ALPHA-2.
FT      CARBOHYD      111      111      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      VARSPLIC      360      376      Missing (in isoform 2).
FT                                          /FTId=VSP_006164.
SQ      SEQUENCE      661 AA; 73663 MW; E6359C1F95C3AB3E CRC64;

```

```

Query Match          6.3%; Score 203.5; DB 1; Length 661;
Best Local Similarity 22.3%; Pred. No. 5.6e-07;

```

Matches 128; Conservative 91; Mismatches 204; Indels 151; Gaps 28;

```

Qy      39 PSTGQNNESCSGSSDCKEGVILPIWYPENP-SLGD-KIARVIVYFVALIYMFLGVSIIAD 96
      | : || | :| :| ||:: || : : :|:: : ||| : :| : |
Db      101 PPLSKEGES-ENSTDHAQGD-----YPKDIFSLEERRKGAILLHVIGMIYMFIALAIVCD 154

Qy      97 R-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEV 155
      |: |: ||| : : : :| : | || | ||| : ||| |
Db      155 EFFVPSLTVITEK-----LGI-SDDVAGATFMAAGGSAPELFTSLIGV 196

Qy      156 CGHGFIA-GDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAY 214
      ||| :| ||||| ||: :||:| :|:| :| :| :|
Db      197 ----FIAHSNVGIGTIVGSAVFNILFVIGMCALF-----SREILNL-----TWWPLFRD 241

Qy      215 IWLY-----MILAVFSPGVVQWEGLLTL-FFFPVCVLL-----AWVADKRLLFYKYM 261
      : | :| : | :| || || | :| | : || |:: :
Db      242 VSFYIVDLIMLIIFFLDNVIMWWESLLLLLTAYFCYVVMKFNQVEKWV--KQMINRNKV 299

Qy      262 HKKYRTDKHRGIIIETEGDHP-----KGIEMDGKMMNSH--FLDGNLVPLEGKEVDESRR 314
      | : :| | : :| :| : :| : :|
Db      300 VKVTAPEAQAKPSAARDKDEPTLPKPRQLRGGSASLHNSLMRNSIFQL----- 349

Qy      315 EMIRILKDLKQKHPEKDLDQLVEMANYYALSHQOKSRAFYRIQATRMMTGAGNILKKHAA 374
      || | | : :| :| :| :| :| :| :| :|
Db      350 -MIHTLDPLAE-----ELGSYGKLYYD-----TMTEEGRFREKASI 385

Qy      375 --EQAKKASSMSEVHTDEPE-----DFISKVFFDPCSQCLENCGAVLLTVVRKGGDMS 426
      : ||| : | || | : :| : :| : :| :| :|
Db      386 LHKIAKK-----KCHVDENERQNGAANHVEKIELPNSTSTDVEMTPSSDASEPVQNGNLS 440

Qy      427 KTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSN 486
      : :| : || | : :| ||| : :| :| :| :| :|
Db      441 HNI-----EGAEAQTAEEDQPLSLAWPSETRKQVTFLIVFPIVFP----LWITLPD 489

Qy      487 VRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTI----HVS 542
      || : : | | : :| :| :| :| :| :| :|
Db      490 VR--KPSSRKFFPITFFGSI-----TWIAVFSYLMVWWAHQVG 525

Qy      543 ESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGG 576
      |:|:| : | | || | | :| :|
Db      526 ETIGISEEIMGLTILAAGTSIPDLITSVIVARKG 559

```

RESULT 14

NKX1_RAT

ID NKX1_RAT STANDARD; PRT; 1181 AA.

AC Q9QZM6; Q62932;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-

DE exchange protein 1) (Retinal rod Na-Ca+K exchanger).

GN SLC24A1 OR NCKX1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

```

RN      [1]
RP      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC      STRAIN=Sprague-Dawley; TISSUE=Eye;
RX      MEDLINE=20217335; PubMed=10751314;
RA      Poon S., Leach S., Li X.-F., Tucker J.E., Schnetkamp P.P.M.,
RA      Lytton J.;
RT      "Alternatively spliced isoforms of the rat eye
RT      sodium/calcium+potassium exchanger NCKX1.";
RL      Am. J. Physiol. 278:C651-C660(2000).
RN      [2]
RP      SEQUENCE OF 1067-1155 FROM N.A.
RA      White K.E., Gesek F.A., Friedman P.A.;
RL      Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
CC      -!- FUNCTION: Critical component of the visual transduction cascade,
CC      controlling the calcium concentration of outer segments during
CC      light and darkness. Light causes a rapid lowering of cytosolic
CC      free calcium in the outer segment of both retinal rod and cone
CC      photoreceptors and the light-induced lowering of calcium is caused
CC      by extrusion via this protein which plays a key role in the
CC      process of light adaptation. Transports one Ca(2+) and one K(+) in
CC      exchange for four Na(+).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=4;
CC          Name=1;
CC              IsoId=Q9QZM6-1; Sequence=Displayed;
CC          Name=2;
CC              IsoId=Q9QZM6-2; Sequence=VSP_006161;
CC          Name=3;
CC              IsoId=Q9QZM6-3; Sequence=VSP_006162;
CC          Name=4;
CC              IsoId=Q9QZM6-4; Sequence=VSP_006163;
CC      -!- TISSUE SPECIFICITY: Highly expressed in the eye.
CC      -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF176688; AAD53121.1; -.
DR      EMBL; U49235; AAB37753.1; -.
DR      InterPro; IPR004817; K_NaCaexchang.
DR      InterPro; IPR004481; K_NaCaexchn.
DR      InterPro; IPR004837; NaCa_Exmemb.
DR      Pfam; PF01699; Na_Ca_Ex; 2.
DR      TIGRFAMs; TIGR00927; 2A1904; 1.
DR      TIGRFAMs; TIGR00367; TIGR00367; 1.
KW      Vision; Transport; Antiport; Symport; Calcium transport;
KW      Transmembrane; Glycoprotein; Phosphorylation; Signal; Repeat;
KW      Alternative splicing.
FT      SIGNAL          1      38      POTENTIAL.
FT      CHAIN           39     1181     SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
FT      DOMAIN          39      419     EXTRACELLULAR (POTENTIAL).

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FT	TRANSMEM	420	440	POTENTIAL.
FT	DOMAIN	441	464	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	465	485	POTENTIAL.
FT	DOMAIN	486	491	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	492	512	POTENTIAL.
FT	DOMAIN	513	519	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	520	544	POTENTIAL.
FT	DOMAIN	545	552	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	553	569	POTENTIAL.
FT	DOMAIN	570	989	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	990	1010	POTENTIAL.
FT	DOMAIN	1011	1017	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1018	1038	POTENTIAL.
FT	DOMAIN	1039	1053	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1054	1074	POTENTIAL.
FT	DOMAIN	1075	1092	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1093	1113	POTENTIAL.
FT	DOMAIN	1114	1121	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1122	1142	POTENTIAL.
FT	DOMAIN	1143	1150	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1151	1171	POTENTIAL.
FT	DOMAIN	1172	1181	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	461	501	ALPHA-1.
FT	REPEAT	1061	1092	ALPHA-2.
FT	DOMAIN	730	905	14 X APPROXIMATE TANDEM REPEATS.
FT	REPEAT	730	741	1.
FT	REPEAT	742	754	2.
FT	REPEAT	755	766	3.
FT	REPEAT	767	778	4.
FT	REPEAT	779	791	5.
FT	REPEAT	792	804	6.
FT	REPEAT	805	817	7.
FT	REPEAT	818	830	8.
FT	REPEAT	831	843	9.
FT	REPEAT	844	856	10.
FT	REPEAT	857	869	11.
FT	REPEAT	870	881	12.
FT	REPEAT	882	893	13.
FT	REPEAT	894	905	14.
FT	DOMAIN	952	974	POLY-GLU.
FT	MOD_RES	625	625	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	271	271	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	598	710	Missing (in isoform 2).
FT				/FTId=VSP_006161.
FT	VARSPLIC	616	710	Missing (in isoform 3).
FT				/FTId=VSP_006162.
FT	VARSPLIC	652	679	Missing (in isoform 4).
FT				/FTId=VSP_006163.
SQ	SEQUENCE	1181 AA;	129980 MW;	B063C1C1193696AE CRC64;

Query Match 6.3%; Score 203; DB 1; Length 1181;
 Best Local Similarity 20.7%; Pred. No. 1.3e-06;
 Matches 134; Conservative 89; Mismatches 207; Indels 216; Gaps 29;

Qy	77	VIVYFVALIYMFLGVSIIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN	135
		::: : : : :: : : :: : :: : :	
Db	422	VVLHIFGMTYVFVALAIVCDEYFVPALGVITDK-----LQI-SEDVAG	463

QY 136 LTIMALGSSAPEILLSLIEVCGHGFA-GDLGPSTIVGSAAFMFIIGICVYVIPDGET 194
 | | | | | : | | | | | : : | | | | | : : | | :
 Db 464 ATFMAAGGSAPLEFTSLIGV----FISHSNVGIGTIVGSAVFNILFVIGTCALF-----S 514

QY 195 RKIKHLRVFFITAAWSIFAYIWLY-----MILAVFSPGVVQVWEGLLTLFFFPVCV---- 245
 | : | : | | : | : | | : | : | | | : : |
 Db 515 REILNL-----TWWPLFRDVSEFYILDLSMLIVFFLDLSLIAWWESLLLLLAYALYVFTMK 568

QY 246 ----LLAWVADK--RLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEM-----DGK 290
 : | | : : | | : | | | | : : :
 Db 569 WNKQIERWVKEQLSRPVAKVMA LGDLSKPSDGAIEENEQQDNKKLKLPSVLTRGSSSSAS 628

QY 291 MMNS-----HFLDGNLVPL----EGKEVDESRRMIRILKDLK-----QKHP----- 328
 : | | : : | | : | | : | | : : |
 Db 629 LHSNIIRSTIYHMLHSLDPLGEARPSKDKQESLNQEARVLPQTKAESSSSDEEEPAELPA 688

QY 329 -----EKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGN 367
 : : | : : : : : : : : :
 Db 689 VTVTPAPAPEDKGDQEEDPGCQEDVD EAEHRGDMTGEEGERETEA---EGKKDEEGETE 744

QY 368 ILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSK 427
 : | : : : | | : | | : | |
 Db 745 AERKEDGQEEETETKGEKQEGETES-----EGKD--- 774

QY 428 TMYVDYKTEDGSANAGADYE---FTEGTVVLKPGETQKEFSVGIIDDDIFE----- 475
 : : | : | : | | | | | : | : |
 Db 775 ----EQEGETEAEKGADHEGETEAEKGKEVEHEGETEAE---GTEDEQEGETEAEKGKEVE 827

QY 476 -----EDEHFFVRLSNVRIEEEQPE---EGMPPAIFNSLPLPRAVLASPCVATVT 522
 | | | | | : | | | |
 Db 828 QEGETEAEKGKEVEH-----EVETEAEKRNHEGETEAEKG----- 863

QY 523 ILDDDHAGIFTFECDTIH--VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDF 580
 : | | | : | : | : | : : : : | : : |
 Db 864 --EADHEGETEAEGNVEHQGETEAEKGVEHEGETEAGEKD-----EHEGQSETQADDT 914

QY 581 E--DTYGELEFKNDETVC DRQEADYGRRG-----QEDSRD 614
 | | | | | : : : | | : | |
 Db 915 EVKDGEAE-ANAEDQCETAQGEKGADGGGSDGGDSEEEDEED 959

RESULT 15

NKX2_RAT

ID NKX2_RAT STANDARD; PRT; 670 AA.

AC 054701; 054706;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sodium/potassium/calcium exchanger 2 precursor (Na(+)/K(+)/Ca(2+)-exchange protein 2) (Retinal cone Na-Ca+K exchanger).

GN SLC24A2 OR NKX2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=98129830; PubMed=9461611;
 RA Tsoi M., Rhee K.-H., Bungard D., Li X.-F., Lee S.-L., Auer R.N.,
 RA Lytton J.;
 RT "Molecular cloning of a novel potassium-dependent sodium-calcium
 RT exchanger from rat brain.";
 RL J. Biol. Chem. 273:4155-4162(1998).
 CC -!- FUNCTION: Critical component of the visual transduction cascade,
 CC controlling the calcium concentration of outer segments during
 CC light and darkness. Light causes a rapid lowering of cytosolic
 CC free calcium in the outer segment of both retinal rod and cone
 CC photoreceptors and the light-induced lowering of calcium is caused
 CC by extrusion via this protein which plays a key role in the
 CC process of light adaptation. Transports one Ca(2+) and one K(+) in
 CC exchange for four Na(+).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O54701-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O54701-2; Sequence=VSP_006165;
 CC -!- TISSUE SPECIFICITY: Expressed abundantly in all regions of the
 CC brain and weakly in the eye, large intestine and adrenal tissue.
 CC -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; AF021923; AAC19405.1; -.
 DR EMBL; AF027506; AAC19404.1; -.
 DR InterPro; IPR004481; K_NaCaexchg.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR TIGRFAMs; TIGR00367; TIGR00367; 1.
 KW Vision; Transport; Antiport; Symport; Calcium transport;
 KW Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
 KW Signal; Repeat; Alternative splicing.
 FT SIGNAL 1 58 POTENTIAL.
 FT CHAIN 59 670 SODIUM/POTASSIUM/CALCIUM EXCHANGER 2.
 FT DOMAIN 59 133 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 134 154 POTENTIAL.
 FT DOMAIN 155 179 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 180 200 POTENTIAL.
 FT DOMAIN 201 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 226 POTENTIAL.
 FT DOMAIN 227 244 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 245 265 POTENTIAL.
 FT DOMAIN 266 266 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 267 287 POTENTIAL.
 FT DOMAIN 288 478 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	479	499	POTENTIAL.
FT	DOMAIN	500	506	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	507	527	POTENTIAL.
FT	DOMAIN	528	542	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	543	563	POTENTIAL.
FT	DOMAIN	564	578	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	579	599	POTENTIAL.
FT	DOMAIN	600	611	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	612	632	POTENTIAL.
FT	DOMAIN	633	639	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	640	660	POTENTIAL.
FT	DOMAIN	661	670	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	175	215	ALPHA-1.
FT	REPEAT	550	581	ALPHA-2.
FT	CARBOHYD	112	112	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	360	376	Missing (in isoform 2).
FT				/FTid=VSP_006165.
FT	CONFLICT	309	309	Q -> R (IN REF. 1; AAC19404).
SQ	SEQUENCE	670 AA;	74656 MW;	4E855A467FC6679E CRC64;

Query Match 6.2%; Score 201.5; DB 1; Length 670;
 Best Local Similarity 24.2%; Pred. No. 7.9e-07;
 Matches 102; Conservative 67; Mismatches 128; Indels 125; Gaps 25;

Qy	39	PSTGQNNESCSGSSDCKEGVILPIWYPENP-SLGD-KIARVIVYFVALIYMFLGVSIAD	96
Db	102	PPASQEDRSENG-TDHAQGD-----YPKDVSLEERRKGAILHVIGMIYMFIALAIVCD	155
Qy	97	R-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEV	155
Db	156	EFFVPSLTVITEK-----LGI-SDDVAGATFMAAGGSAPELFTSLIGV	197
Qy	156	CGHGFIGA-GDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAY	214
Db	198	----FIAHSNVGIGTIVGSAFVNILFVIGMCALF-----SREILNL-----TWWPLFRD	242
Qy	215	IWLY-----MILAVFSPGVVQVWEGLLTL-FFFPVCVLL-----AWVADKRLLFYKYM	261
Db	243	VSFYIVDLIMLIIFFLDNVIMWWESLLLLTAYFAYVVFMMKFNVQVERWV-----	291
Qy	262	HKKYRTDKHRGIII-----ETEGD-----HPKGIEMDGK-----MMNS---	294
Db	292	--KQMINRNKVVKVTVSEAQAQASTAGDKEEPTLPNKPRLQGGSSASLHNSLMRNSIFQ	349
Qy	295	---HFLDGNLVPLE-----GK-----EVDESIR-REMIRILKDLKQKHPEKDLDQ----	334
Db	350	LMIHTLD----PLAEELGSYGKLYYDTMTTEGRFREKASILHAKKCCQVDENERQNG	405
Qy	335	LVE MANYYALSHQQKSRAFYRIQATRMMTGA-----GNILKKHAAEQAKKASSMSEVHTD	389
Db	406	AANHVDYAAEKIELPNSTSTEVEMTSPSEASEPVQNGNLSHSIEAADAPQATETAEDDD	465
Qy	390	EP	391
Db	466	QP	467

Search completed: June 24, 2004, 16:12:40
Job time : 12.6677 secs